

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2003, 03:48:42 ; Search time 614 Seconds

(without alignments)
8137.882 Million cell updates/sec

Title: US-09-308-830A-12

Perfect score: 1851

Sequence: 1 ccatcgcgcacatcatgt.....tttagcaactatttcgtc 1851

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_19Jun03.*

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24: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
25: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1851	100.0	1851	AAAT51716	Streptococcus pyog
2	1851	100.0	1851	AAV41593	Nucleotide sequenc
3	1835.4	99.2	1837	AAAT28540	S. pyogenes detect
4	1835.4	99.2	1837	ABA76857	Streptococcus pyog
5	1832.2	99.0	1837	AAAT51112	Streptococcus pyro
6	1832.2	99.0	1837	ABN84229	Streptococcal pyro
7	754.4	40.8	756	AAH01002	Unidentified nucle
8	184.2	10.0	1712	AAAT51107	Staphylococcal ent

c	9	184.2	10.0	1712	24	ABN84224	Staphylococcal ent
10	178.8	9.7	2155561	24	ABN71527	Streptococcus poly	
11	176.2	9.5	1712	21	AAAT51108	Mutant Staphylococ	
12	176.2	9.3	1712	24	ABN84225	Staphylococcal ent	
13	171.4	9.3	773	18	AAAT45698	Staphylococcal ent	
14	164.6	8.9	1095	21	AAAT51111	Staphylococcal ent	
15	164.6	8.9	1095	24	ABN84228	Staphylococcal SEC	
16	161.2	8.7	723	21	AAAT45835	Mutant SEB gene en	
17	161.2	8.7	801	21	AAAT45834	Mutant SEB gene en	
18	161.2	8.7	1388	21	AAAT51109	Mutant Staphylococ	
19	161.2	8.7	1388	24	ABN84226	Staphylococcal ent	
20	159.6	8.6	867	22	AAAT74983	Nucleotide sequenc	
21	145.8	7.9	177	24	ABN66731	Streptococcus poly	
22	126.2	7.1	186	24	ABN66706	Streptococcus poly	
23	126.2	6.8	141	10	AAAT90259	Human alpha-interf	
24	112.4	6.1	815	21	AAAT09240	Plant-optimized mu	
25	107.6	5.8	180	24	ABN66707	Streptococcus poly	
26	84.2	4.5	8056	25	ABAT10246	Haematopoietic cel	
27	84	4.5	8056	25	ABAT10246	Haematopoietic cel	
28	75.6	4.1	8056	25	ABAT10100	Haematopoietic cel	
29	74	4.0	8056	25	ABAT10100	Haematopoietic cel	
30	72.8	3.9	757	21	AAAT51106	Mutant Staphylococ	
31	72.8	3.9	757	21	AAAT45833	Mutant SEA gene en	
32	72.8	3.9	757	24	ABN84223	Staphylococcal ent	
33	72.8	3.9	830	21	AAAT51105	Staphylococcal ent	
34	72.8	3.9	830	24	ABN84222	Staphylococcal ent	
35	72.8	3.9	7131	24	ABAT70427	Chemically treated	
36	72.8	3.9	7131	24	AAAT61360	Human gene regulat	
37	72.8	3.9	7131	24	AAAT31450	Signal transductio	
38	71	3.8	6131	24	ABAT32891	Human immune syste	
39	70.6	3.8	626	23	ABAT60941	Human prostate exp	
40	70.4	3.8	14919	22	AAAT46506	Tumour suppressor	
41	70	3.8	15548	24	ABAT34155	Human immune syste	
42	69.4	3.7	494	23	ABAT10021	Human prostate exp	
43	68.2	3.7	50000	24	ABAT56202	AmEPV genome fragm	
44	68	3.7	18683	24	ABAT54334	Chemically treated	
45	68	3.7	18683	24	ABAT32313	Human immune syste	

ALIGNMENTS

RESULT 1
AAAT51716
ID AAAT51716 standard; DNA; 1851 BP.

XX AAAT51716;

AC AAAT51716;

XX 04-NOV-1997 (first entry)

DE Streptococcus pyogenes Streptococcal toxin A DNA.

XX Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
KW vaccine; protection; treatment; cancer; neutralising antibody;
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration;
KW fever; hypotension; group A streptococcal infection; myositis;
KW fascitis; liver damage; T cell; lymphoma; ovarian; uterine; ss.

XX Streptococcus pyogenes.

XX Key Location/Qualifiers

FT FH 828..1583

FT CDS /*tag= a

FT sig_peptide 828..917

FT /*tag= b

FT mat_peptide /*tag= c

FT /product= Streptococcal_toxin_A

XX W09640930-A1.

XX 19-DEC-1996.

XX

PF	07-JUN-1996;	96WO-US10252.	1541	TCGCTACTGTGTCACCTAAATATATACCCCTTATCAATGCTCTCTTTAACTCATCTATAT	600
XX					
PR	07-JUN-1995;	95US-0480261.	541	TCGCTACTGTGTCACCTAAATATATACCCCTTATCAATGCTCTCTTTAACTCATCTATAT	600
XX					
PA	(MINU)	UNIV MINNESOTA.	601	ATAACATATTTTCATCTCCTACCTATCTATTCGTAAAAAGATAAAAAATAACTATTGTTTT	660
XX					
PI	Ohlendorf D, Roggliani M, Schlievert PM, Stoehr J;		601	ATAACATATTTTCATCTCCTACCTATCTATTCGTAAAAAGATAAAAAATAACTATTGTTTT	660
XX					
DR	WPI: 1997-099936/09.		661	TTTTGTTATTTTAAATAAAATTAATAATAAGTAATGTTTTTAAAAAATATACAAT	720
DR	P-PSDB; AAW12097.				
XX			661	TTTTGTTATTTTAAATAAAATTAATAATAAGTAATGTTTTTAAAAAATATACAAT	720
XX					
PT	Mutant SPE-A toxin with at least one amino acid change is		721	TTATCTTATTTATAGTTAGCTATTTTTCATTTAGTAAATATTTGGTGAATTTGTAATAAC	780
PT	substantially non-lethal - used in vaccine composition for				
PT	treatment of cancer and streptococcal toxic shock syndrome etc.		721	TTATCTTATTTATAGTTAGCTATTTTTCATTTAGTAAATATTTGGTGAATTTGTAATAAC	780
XX					
PS	Disclosure; Pages 77-79; 102pp; English.				
XX			781	CTTTTAAATCTAGAGGAGAACCCAGATATATAATGGAGGAATTAATTTGGAACAATA	840
CC	The present sequence encodes Streptococcus pyogenes Streptococcal				
CC	toxin A (SPE-A), from which a non-lethal mutant SPE-A, comprising		781	CTTTTAAATCTAGAGGAGAACCCAGATATATAATGGAGGAATTAATTTGGAACAATA	840
CC	at least 1 amino acid change, can be derived. The mutant SPE-A can				
CC	be used to produce vaccines to protect animals against wild type		841	AAAAAGTATTTGAAGAAAATGATTTTGTGTTTGTAGTGACATTTCTTTGGACTAAACAATCT	900
CC	SPE-A and to treat cancer and streptococcal toxic shock syndrome				
CC	(STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be		841	AAAAAGTATTTGAAGAAAATGATTTTGTGTTTGTAGTGACATTTCTTTGGACTAAACAATCT	900
CC	produced, which may be used to ameliorate STSS symptoms, e.g.				
CC	fever, hypotension, group A streptococcal infection, myositis,		901	CGCAAGAGTATTTGCTCAACAGACCCCGATCCCAAGCAACTTTCACAGATCTAGTTAG	960
CC	faciitis and liver damage. The neutralising Ab is preferably,				
CC	administered in conjunction with antibiotic therapy. The mutant		901	CGCAAGAGTATTTGCTCAACAGACCCCGATCCCAAGCAACTTTCACAGATCTAGTTAG	960
CC	SPE-A is especially useful for treating T cell lymphomas, and				
CC	ovarian and uterine cancer. It is thought that mutant SPE-A can be		961	TTAAAAACCTTCAAAATATATATTTTCTTTATGAGGGTGCCTGTTACTCACAGAGATG	1020
CC	selectively toxic to T cell lymphoma cells.				
XX			961	TTAAAAACCTTCAAAATATATATTTTCTTTATGAGGGTGCCTGTTACTCACAGAGATG	1020
SQ	Sequence 1851 BP; 635 A; 326 C; 248 G; 642 T; 0 other;				
	Query Match	100.0%; Score 1851; DB 18; Length 1851;			
	Best Local Similarity	100.0%; Pred. No. 2.6e-286;			
	Matches 1851; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	CCATCAGCATCACTCATGTTTGACAGCTTATCATCGATAAGCTTACTTTTCAATCAGG	60		
DB					
QY	1	CCATCAGCATCACTCATGTTTGACAGCTTATCATCGATAAGCTTACTTTTCAATCAGG	60		
DB					
QY	61	TCATCTCTTGAACAGGTGCAACATAGATTAGGCGATGGAGATTTACAGACAATATGA	120		
DB					
QY	61	TCATCTCTTGAACAGGTGCAACATAGATTAGGCGATGGAGATTTACAGACAATATGA	120		
DB					
QY	121	ACGTATATCTACATCAGCAATCGCAATTGATGACATTTGGAACATAAATCAATCAAT	180		
DB					
QY	121	ACGTATATCTACATCAGCAATCGCAATTGATGACATTTGGAACATAAATCAATCAAT	180		
DB					
QY	181	TTGTTTACTAACAGCAACTAGATTGACAACATAATTCACAACAGGTTAATTTAACACA	240		
DB					
QY	181	TTGTTTACTAACAGCAACTAGATTGACAACATAATTCACAACAGGTTAATTTAACACA	240		
DB					
QY	241	TTCAAGTAACTCCACAGCTCCATCAATGCTTACCGTAAGTAATCAATAACTTACTAAA	300		
DB					
QY	241	TTCAAGTAACTCCACAGCTCCATCAATGCTTACCGTAAGTAATCAATAACTTACTAAA	300		
DB					
QY	301	CCTTGTACATCAAGGTTTTTCTTTTGTCTGTCATGAGTTACCAATCACTTTCTATA	360		
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QY	301	CCTTGTACATCAAGGTTTTTCTTTTGTCTGTCATGAGTTACCAATCACTTTCTATA	360		
DB					
QY	361	TTATTGACAACATAAATTGACAACCTCTTCAATTAATTTTCTGCTACTCAAAAGTTTCTTC	420		
DB					
QY	361	TTATTGACAACATAAATTGACAACCTCTTCAATTAATTTTCTGCTACTCAAAAGTTTCTTC	420		
DB					
QY	421	ATTGATATAGTCTAATTTCCACATCACTCTTCCACTCTCTCTACCGTCAACAATTCAT	480		
DB					
QY	421	ATTGATATAGTCTAATTTCCACATCACTCTTCCACTCTCTCTACCGTCAACAATTCAT	480		
DB					
QY	481	CATCTCTCACTTTTTGTGTTGTAACATATCAATATCTTCCGTTTTTACGGACTA	540		
DB					
QY	481	CATCTCTCACTTTTTGTGTTGTAACATATCAATATCTTCCGTTTTTACGGACTA	540		
DB					


```

Db      1021 TGAATCTGTGTGATCAACTTTTATCTCACCATTAAATATATATATGTTTCAGGGCCAAATT 1080
QY      1081 ATGATAAATTAATAAAGTCACTTAAAGAACAGAGATGGCAACTTTATTTAAGGATAAAA 1140
Db      1081 ATGATAAATTAATAAAGTCACTTAAAGAACAGAGATGGCAACTTTATTTAAGGATAAAA 1140
QY      1141 ACCTTGATATTTATGGTGTAGAAATATTACCATCTCTCTGTTATTTATGTAAGAAATGAGAAA 1200
Db      1141 ACCTTGATATTTATGGTGTAGAAATATTACCATCTCTCTGTTATTTATGTAAGAAATGAGAAA 1200
QY      1201 GGAGTCATGTATCTACGGAGGGGTAACAATCATGATGAAGGAAATCATTTAGAAATTCCTA 1260
Db      1201 GGAGTCATGTATCTACGGAGGGGTAACAATCATGATGAAGGAAATCATTTAGAAATTCCTA 1260
QY      1261 AAAAGATAGTCTTAAAGTATCAATCGATGGTGTATCCAAAGCCATCATTTGATATGTAAG 1320
Db      1261 AAAAGATAGTCTTAAAGTATCAATCGATGGTGTATCCAAAGCCATCATTTGATATGTAAG 1320
QY      1321 CAATATAAATAATGTAAGTCTCAAGAAATAGACTATAAAGTTAGAAATATCTTACAG 1380
Db      1321 CAATATAAATAATGTAAGTCTCAAGAAATAGACTATAAAGTTAGAAATATCTTACAG 1380
QY      1381 ATATTAAGCACTATATACATAAGTGGACCTTCTAATATGAATGAACCTGGATATATAAGTTCA 1440
Db      1381 ATATTAAGCACTATATACATAAGTGGACCTTCTAATATGAATGAACCTGGATATATAAGTTCA 1440
QY      1441 TACCTAAGATAAAGAAAGTTTGTGTTGATTTTCCCTGAACAGCAATTTACTCAAT 1500
Db      1441 TACCTAAGATAAAGAAAGTTTGTGTTGATTTTCCCTGAACAGCAATTTACTCAAT 1500
QY      1501 CTAAATATCTTATGATATATAAAGATAATGAACGCTTGACTCAAAACAGCCAAATG 1560
Db      1501 CTAAATATCTTATGATATATAAAGATAATGAACGCTTGACTCAAAACAGCCAAATG 1560
QY      1561 AAGTCTACCTAACCAAGTACATTTTGTGTTTGGCAACCTTACCTACTGCTGGATTT 1620
Db      1561 AAGTCTACCTAACCAAGTACATTTTGTGTTTGGCAACCTTACCTACTGCTGGATTT 1620
QY      1621 AGAAATTTTATGCAATCTTTTATTAATGTAATAAAGCGCTCATTTGATGAGCGGTTTG 1680
Db      1621 AGAAATTTTATGCAATCTTTTATTAATGTAATAAAGCGCTCATTTGATGAGCGGTTTG 1680
QY      1681 TCTTATCTAAGGAGCTTTACCTCTTAATGTCGCAAAATTTTAAATGTTGGATTTTGA 1740
Db      1681 TCTTATCTAAGGAGCTTTACCTCTTAATGTCGCAAAATTTTAAATGTTGGATTTTGA 1740
QY      1741 TTTGCTATTTGTTATGATGGTAATCCCATTTTTCGACAGACATCGTGGCCACCTCT 1800
Db      1741 TTTGCTATTTGTTATGATGGTAATCCCATTTTTCGACAGACATCGTGGCCACCTCT 1800
QY      1801 AACACAAATCATAGACAGAGCTTTAGCTTAGCAACTATTTTATCGTC 1851
Db      1801 AACACAAATCATAGACAGAGCTTTAGCTTAGCAACTATTTTATCGTC 1851

```

RESULT 3

AAT28540

ID AAT28540 standard; DNA; 1837 BP.

AC AAT28540;

XX AAT28540;

XX AAT28540;

DT 02-APR-1997 (first entry)

DE S. pyogenes detection probe #2.

XX S. pyogenes detection probe #2.

XX S. pyogenes detection probe #2.

KW Detection; probe; amplification primer; bacterial pathogen; pneumonia;

KW Escherichia coli; Klebsiella pneumoniae; Pseudomonas aeruginosa;

KW Proteus mirabilis; Streptococcus pneumoniae; Staphylococcus aureus;

KW Staphylococcus epidermidis; Enterococcus faecalis; respiratory tract;

KW Staphylococcus saprophyticus; Streptococcus pyogenes; urinary tract;

KW Haemophilus influenzae; Moraxella catarrhalis; septicaemia; meningitis;

KW infection; intra-abdominal infection; skin infection;

bacterial resistance; beta-lactam antibiotic; ds.

Synthetic.

WO9608582-A2.

21-MAR-1996.

12-SEP-1995; 95WO-CA00528.

12-SEP-1994; 94US-0304732.

(BERG/) BERGERON M G.

(OUEL/) OUELLETTE M.

(ROY/) ROY P H.

Bergeron MG, Ouellette M, Roy PH;

WPI; 1996-179953/18.

Method for the detection of bacterial species using probes and

primers - allows detection and quantification of antibiotic

resistant bacteria in patients, the environment and food

Claim 57; Page 92-93; 216pp; English.

The sequences given in AAT28539-40 represent probes which were used in the method of the invention for the detection of *S. pyogenes* in a sample. The method comprises using probes and/or amplification primers which are specific, ubiquitous and sensitive for determining the presence and/or amount of nucleic acids from selected bacterial species in any sample, where the bacterial nucleic acid comprises a selected target region hybridisable with the probes or primers. The method comprises contacting the sample with the probes or primers and detecting the presence and/or amount of hybridised primers or amplification products as an indication of the presence and/or amount of the bacterial species. This method may be used to detect commonly encountered bacterial pathogens, e.g. *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Proteus mirabilis*, *Streptococcus pneumoniae*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Enterococcus faecalis*, *Staphylococcus saprophyticus*, *Streptococcus pyogenes*, *Haemophilus influenzae* and *Moraxella catarrhalis*. These bacterial species are associated with approx. 90% of urinary tract infections and with a high percentage of other severe infections including septicaemia, meningitis, pneumonia, intra-abdominal infections, skin infections and other severe respiratory tract infections. The method may also be used to evaluate a bacterial resistance to beta-lactam antibiotics.

Sequence 1837 BP; 631 A; 318 C; 248 G; 640 T; 0 other;

Query Match 99.2%; Score 1835.4; DB 17; Length 1837;
 Best Local Similarity 99.9%; Pred. No. 8.3e-286;
 Matches 1836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 TCATGTTTGACAGCTTATCATCGATAAGCTTACTTTTCGATAGGCTCTATCTGTAAC 74

Db 1 TCATGTTTGACAGCTTATCATCGATAAGCTTACTTTTCGATAGGCTCTATCTGTAAC 60

QY 75 AGGTGCAACATAGATTAGGCGCATGAGATTACCAACAACATATGACAGTATATACAC 134

Db 61 AGGTGCAACATAGATTAGGCGCATGAGATTACCAACAACATATGACAGTATATACAC 120

QY 135 ATCAGCAATTCGCAATTCATGACATTTGGAACCTAAATTCATCAATTTGTTACTACAAG 194

Db 121 ATCAGCAATTCGCAATTCATGACATTTGGAACCTAAATTCATCAATTTGTTACTACAAG 180

QY 195 CAACTAGATTGACACTTAATTCCTCAACAACAGTTTAATTTACACATTTCAAGTAACTCC 254

Db 181 CAACTAGATTGACACTTAATTCCTCAACAACAGTTTAATTTACACATTTCAAGTAACTCC 240

QY 255 ACCAGCTCCATCAATGCTTACCGTAAGCTATATCACTTACTAAAACCTTTGTACATCAA 314

Db 241 ACCAGTCCATCAATGCTTACCGTAAGTAATCATCACTTACTAAAACCTTGTACATCAA 300
 QY 315 GGTGTTTTCTTTTGTCTTGTTCATGAGTTACCAATAAAGTTCTATATATTTGACAACTAA 374
 Db 301 GGTGTTTTCTTTTGTCTTGTTCATGAGTTACCAATAAAGTTCTATATATTTGACAACTAA 360
 QY 375 ATTGCAACTCTTCAATATATTTTCTGCTACTCAAAAGTTTCTTCATTTGATATAGTCT 434
 Db 361 ATTGCAACTCTTCAATATATTTTCTGCTACTCAAAAGTTTCTTCATTTGATATAGTCT 420
 QY 435 AATTCACCATCACTTCTCCACTCTCTACCGTCCACAACCTTCATCATCTCTCACTTTT 494
 Db 421 AATTCACCATCACTTCTCCACTCTCTACCGTCCACAACCTTCATCATCTCTCACTTTT 480
 QY 495 TCGTGTGTAACACATAATCAATATCTTTCCGTTTTTACGCACTATCCCTACTGTGCA 554
 Db 481 TCGTGTGTAACACATAATCAATATCTTTCCGTTTTTACGCACTATCCCTACTGTGCA 540
 QY 555 CCTAAATATACCCCTTATCAATCGTCTTTTAACTCACTATATATATATATATTTTAT 614
 Db 541 CCTAAATATACCCCTTATCAATCGTCTTTTAACTCACTATATATATATATATTTTAT 600
 QY 615 CCTCTACTATCTATTCGTAATAAGATAAATAAATAAATAAATAAATAAATAAATAAATA 674
 Db 601 CCTCTACTATCTATTCGTAATAAGATAAATAAATAAATAAATAAATAAATAAATAAATA 660
 QY 675 AATAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 734
 Db 661 AATAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 720
 QY 735 GTTACTATTTTTCATGTTAGTAATATTTGTTGAATGTAATTAATTAATTAATTAATTAAT 794
 Db 721 GTTACTATTTTTCATGTTAGTAATATTTGTTGAATGTAATTAATTAATTAATTAATTAAT 780
 QY 795 AGGAAACCCAGATATAAATGAGGAGATATTAATGGAATAAATAAATAAATAAATAAATAA 854
 Db 781 AGGAAACCCAGATATAAATGAGGAGATATTAATGGAATAAATAAATAAATAAATAAATAA 840
 QY 855 AAAATGGTATTTTGTGTTAGTACATTTCTGGACTAACATCTCGCAAGAGGTATTT 914
 Db 841 AAAATGGTATTTTGTGTTAGTACATTTCTGGACTAACATCTCGCAAGAGGTATTT 900
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 QY 975 AATATATATTTTCTTTATGAGGAGTCACTGTTTACTCAGGAGAACTGGAATCTGTTGAT 1034
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 QY 1095 ACTGAACCTTGAACAACAGAGATGGAACCTTTTATTAAGGATAAACAAGCTTGATATTTAT 1154
 Db 1081 ACTGAACCTTGAACAACAGAGATGGAACCTTTTATTAAGGATAAACAAGCTTGATATTTAT 1140
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 QY 1335 GTAACGTCAAGAAATTAAGTATATAAAGTTAGAAATATCTTTACAGATAAATAAGCAACTA 1394
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 QY 1755 TTGATGGGTAATCCCAATTTTTCGACAGACATCGTGGCCACCTCTAAACACCAAAATCAT 1814
 Db 1741 TTGATGGGTAATCCCAATTTTTCGACAGACATCGTGGCCACCTCTAAACACCAAAATCAT 1800
 QY 1815 AGACAGGAGCTTGTAGCTTAGCCTAGCACTATTTTATCGTC 1851
 Db 1801 AGACAGGAGCTTGTAGCTTAGCAACTATTTTATCGTC 1837

RESULT 4

ABA76857 ID ABA76857 standard; DNA; 1837 BP.
 XX ABA76857;
 DT 28-JAN-2002 (first entry)
 XX Streptococcus pyogenes polynucleotide SEQ ID NO 33.
 DE Detection; bacterial species; animal; food; environment;
 KW antibiotic resistance; ds.
 XX Streptococcus pyogenes.
 OS NZ501596-A.
 PN 29-JUN-2001.
 XX 12-SEP-1995; 95NZ-0501596.
 XX 12-SEP-1995; 95NZ-0501596.
 PA (IDI-) IDI INFECTION DIAGNOSTIC INC.
 XX Bergeron MG, Ouellette M, Roy PH;
 XX WPI; 2001-615034/71.
 XX Method for detecting target bacterial species in a sample, comprises
 PT detecting the presence or amount of bacterial nucleic acid amplified by
 PT a primer derived from bacterial DNA, specific for the target bacterial
 species
 XX Claim 6; Page 107-108; 168pp; English.
 PS The invention relates to detecting target bacterial species suspected to
 CC be present in a sample, comprising contacting nucleic acids of target
 CC bacterial species with an amplification primer pair derived from a

bacterial DNA fragment (ABA76825-ABA76861) specific for the target bacterial species but ubiquitous for different strains, amplified the nucleic acid and detecting the presence or amount of an amplified sequence as an indication of the presence or amount of the target bacterial species. The invention includes primers and probes (ABA76862-ABA76984) against the target bacterial species, especially *E. coli*, *K. pneumoniae*, *P. aeruginosa*, *P. mirabilis*, *S. pneumoniae*, *S. aureus*, *S. epidermidis*, *E. faecalis*, *S. saprophyticus*, *S. pyogenes*, *H. influenzae*, *M. catarrhalis* and/or group A *Streptococcus* producing exotoxin A gene spe A, suspected to be present in a sample which is obtained from human patients, animals, environment or food, and which consists of one or more bacterial colonies. Oligonucleotide probes and primers complementary to the bacterial genes encoding resistance to antibiotics such as bla(tem), bla(rob), bla(shv), aadB, aacC1, aacC2, aacC3, aacA4, mecA, vanA, vanH, vanX, satA, aacA-aphD, vat, vga, msrA, sul and/or int (ABA76985-ABA77001) are also useful to identify commonly encountered and clinically important resistance genes. The invention provides a rapid method of bacterial identification that can be achieved, which reduces the time currently required for the identification of pathogens in the clinical laboratory.

XX Sequence 1837 BP; 631 A; 318 C; 248 G; 640 T; 0 other;

Query Match	99.2%;	Score 1835.4;	DB 22;	Length 1837;	
Best Local Similarity	99.9%;	Pred. No. 8.3e-286;			
Matches 1836;	Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	15	TCATGTTTGACAGCTTATCATCGATAAGCTTACTTTTCGAATCAGGTCTATCTCTGAAAC	74		
DB	1	TCATGTTTGACAGCTTATCATCGATAAGCTTACTTTTCGAATCAGGTCTATCTCTGAAAC	60		
QY	75	AGGTGCAACATAGATTAGGCGATGGAGATTTACCAGACAACTATGAAGCTATATACTAC	134		
DB	61	AGGTGCAACATAGATTAGGCGATGGAGATTTACCAGACAACTATGAAGCTATATACTAC	120		
QY	135	ATCAGCGAATGGCAATTGATGACATTGGAACTAAATTCATCAATTTGTTTACTACAAAG	194		
DB	121	ATCAGCGAATGGCAATTGATGACATTGGAACTAAATTCATCAATTTGTTTACTACAAAG	180		
QY	195	CAACTAGATTGACAACTAATTTCTCAACAAAGCTTAATTTTAAACAACTCAAGTAACCTCC	254		
DB	181	CAACTAGATTGACAACTAATTTCTCAACAAAGCTTAATTTTAAACAACTCAAGTAACCTCC	240		
QY	255	ACCAGCTCCATCAATGCTTTACCGTAAGTAATCATCACTTACTTAAACCTTGTGTACATCA	314		
DB	241	ACCAGCTCCATCAATGCTTTACCGTAAGTAATCATCACTTACTTAAACCTTGTGTACATCA	300		
QY	315	GGTTTTTCTTTTGTCTGTCATGAGTTTACCAATCACTTCTATATATTATGTGCAACTAA	374		
DB	301	GGTTTTTCTTTTGTCTGTCATGAGTTTACCAATCACTTCTATATATTATGTGCAACTAA	360		
QY	375	ATTGACAACTCTTCAATATTTTCTGCTACTCAAAAGTTTCTTTCATTTGATATAGTCT	434		
DB	361	ATTGACAACTCTTCAATATTTTCTGCTACTCAAAAGTTTCTTTCATTTGATATAGTCT	420		
QY	435	AAATGCCACATCACTTCTTCCACTCTCTACCGTCACAACTTCATCATCTCTCACTTTT	494		
DB	421	AAATGCCACATCACTTCTTCCACTCTCTACCGTCACAACTTCATCATCTCTCACTTTT	480		
QY	495	TCGTGTTGTAACACATAATCAAAATATCTTTCGGTTTTTACGCATATCGCTACTGTGTCA	554		
DB	481	TCGTGTTGTAACACATAATCAAAATATCTTTCGGTTTTTACGCATATCGCTACTGTGTCA	540		
QY	555	CCTAAATATACCCCTTATCAATCGCTTCTTTAACTCATCTATATATAACATATTTTAT	614		
DB	541	CCTAAATATACCCCTTATCAATCGCTTCTTTAACTCATCTATATATAACATATTTTAT	600		
QY	615	CTCTCTACCTATCTATTCGTAAAAAGATAAAAAAATCACTATTTGTTTTGTTATTTAT	674		
DB	601	CTCTCTACCTATCTATTCGTAAAAAGATAAAAAAATCACTATTTGTTTTGTTATTTAT	660		
QY	675	ATAAAATTTAATTAAGTTAATGTTTTTAAAAATATACAAATTTTATCTATTTATA	734		

DB	661	ATAAAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	720		
QY	735	GTTAGCTATTTTTCATTTGTTAGTAATATTTGTTAGTAATTTGTTAGTAATTTGTTAG	794		
DB	721	GTTAGCTATTTTTCATTTGTTAGTAATATTTGTTAGTAATTTGTTAGTAATTTGTTAG	780		
QY	795	AGGAGAACCCAGATATAAAATGAGGAATATTAATGGAACCAATTAATTAATTAATTA	854		
DB	781	AGGAGAACCCAGATATAAAATGAGGAATATTAATGGAACCAATTAATTAATTAATTA	840		
QY	855	AAAATGTTATTTTGTGTTAGTGACATTTCTTGACATTAACAATCTCGCAAGAGTATTT	914		
DB	841	AAAATGTTATTTTGTGTTAGTGACATTTCTTGACATTAACAATCTCGCAAGAGTATTT	900		
QY	915	GCTCAACAGACCCCGATCAACGCAACCTTACAGATCTAGTTAGTTAGTTAGTTAGTT	974		
DB	901	GCTCAACAGACCCCGATCAACGCAACCTTACAGATCTAGTTAGTTAGTTAGTTAGTT	960		
QY	975	AATATATATTTTCTTATGAGGTGACCTGTTACTCACGAGAAATGGAATCTCTTGAT	1034		
DB	961	AATATATATTTTCTTATGAGGTGACCTGTTACTCACGAGAAATGGAATCTCTTGAT	1020		
QY	1035	CAACTTTTATCTCACCATTTAATATATATATGTTTCAGGCCCAATTTATGATAAATAA	1094		
DB	1021	CAACTTTTATCTCACCATTTAATATATATATGTTTCAGGCCCAATTTATGATAAATAA	1080		
QY	1095	ACTGAACCTTAAGAACCAAGAGATGCAACTTTTATTAAGGATAAAACCTTCATATTT	1154		
DB	1081	ACTGAACCTTAAGAACCAAGAGATGCAACTTTTATTAAGGATAAAACCTTCATATTT	1140		
QY	1155	GGTGAGAAATTTACCATCTCTGTTATTTATGTAATGCAAAAGGAGTGCATGTATC	1214		
DB	1141	GGTGAGAAATTTACCATCTCTGTTATTTATGTAATGCAAAAGGAGTGCATGTATC	1200		
QY	1215	TACGAGGGGTAAACAATCATGAAGGGAATCATTTAGAAATTCCTTAAAGATAGTCGTT	1274		
DB	1201	TACGAGGGGTAAACAATCATGAAGGGAATCATTTAGAAATTCCTTAAAGATAGTCGTT	1260		
QY	1275	AAAGTATCAATGATGATGATCAAGGCTTATCATTTTATTAAGGATAAAACCTTCAT	1334		
DB	1261	AAAGTATCAATGATGATGATCAAGGCTTATCATTTTATTAAGGATAAAACCTTCAT	1320		
QY	1335	GTAACCTGCTCAAGAAATTTAGACTATAAAGTGTAGAAATATCTTACAGATAAAGCACTA	1394		
DB	1321	GTAACCTGCTCAAGAAATTTAGACTATAAAGTGTAGAAATATCTTACAGATAAAGCACTA	1380		
QY	1395	TATACATGACCTTCTAAATATGAACCTGATATTAAGTTCATACCTTAAGATAA	1454		
DB	1381	TATACATGACCTTCTAAATATGAACCTGATATTAAGTTCATACCTTAAGATAA	1440		
QY	1455	GAAAGTTTTTGGTTGATTTTTCCTGCAACGCAATTTTACTCAATCTAAATATCTTATG	1514		
DB	1441	GAAAGTTTTTGGTTGATTTTTCCTGCAACGCAATTTTACTCAATCTAAATATCTTATG	1500		
QY	1515	ATATATAAGATAAATGAACGCTTGACTCAACCAACAGCCAAATGGAAGTCTACCTAACA	1574		
DB	1501	ATATATAAGATAAATGAACGCTTGACTCAACCAACAGCCAAATGGAAGTCTACCTAACA	1560		
QY	1575	ACCAAGTAACCTTTTGGCTTTTGGCAACCTTACCTTACCTGCTGGATTTAGAAATTTATGC	1634		
DB	1561	ACCAAGTAACCTTTTGGCTTTTGGCAACCTTACCTTACCTGCTGGATTTAGAAATTTATGC	1620		
QY	1635	AATTCCTTTTAAATGTAACCAACGCTCATTTGATGAGCGGTTTGTCTTATCTTAAAGGA	1694		
DB	1621	AATTCCTTTTAAATGTAACCAACGCTCATTTGATGAGCGGTTTGTCTTATCTTAAAGGA	1680		
QY	1695	GCTTACCTCCTAATGCTGCAAAATTTTAAATGTTGGATTTTGTATTTGTTGTTATTTAT	1754		
DB	1681	GCTTACCTCCTAATGCTGCAAAATTTTAAATGTTGGATTTTGTATTTGTTGTTATTTAT	1740		
QY	1755	TTGATGGGTAAATCCATTTTTCGACAGACATCGTCGCGCCACTCTACACCAAAATCAT	1814		
DB	1741	TTGATGGGTAAATCCATTTTTCGACAGACATCGTCGCGCCACTCTACACCAAAATCAT	1800		

QY 1815 AGACAGAGCTGTAGCTTAGCACTATTTATCGTC 1851
 Db |||||||
 1801 AGACAGAGCTGTAGCTTAGCACTATTTATCGTC 1837

RESULT 5
 AA251112
 ID AA251112 standard; DNA: 1837 BP.

XX AA251112;
 XX
 XX 05-JUN-2000 (first entry)
 XX

Streptococcal pyrogenic exotoxin A (SPE-A) encoding DNA.

Superantigen toxin; SAg; Streptococcal pyrogenic exotoxin A; SPE-A;
 antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;
 cytostatic; antibody; staphylococcal/streptococcal toxin; toxoid; SPEA42;
 diagnosis; treatment; superantigen-associated bacterial infection; ds.
 Streptococcus sp.

Key Location/Qualifiers
 CDS 814..1569
 FT /*tag= a
 FT /product= "Streptococcal pyrogenic exotoxin A (SPE-A)"

W0200009154-A1.

24-FEB-2000.

13-AUG-1998; 98WO-US16766.

13-AUG-1998; 98WO-US16766.

(REED-) REED ARMY INST RES WALTER.

Ulrich RG, Olson MA, Bavari S;

WPI: 2000-224177/19.

P-PSDB: AAY70109.

Nucleic acid encoding superantigen toxin useful as a vaccine and for
 diagnosis of superantigen-associated bacterial infections -
 Example 12; Page 92-94; 118pp; English.

The present sequence is the DNA encoding Streptococcal pyrogenic
 exotoxin A (SPE-A), a bacterial superantigen toxin (SAG), used for the
 formulation of SPE-A vaccine SPEA42. The coding region of this SAG toxin
 is altered by site directed mutagenesis, introducing L42R mutation, that
 results in disruption of binding of the toxin to both the MHC class II
 or T-cell antigen receptor. SPE-A has antibacterial and cytostatic
 activity. This sequence is useful for the production of SPE-A vaccines
 and specific antibodies. This vaccine overcomes the disadvantages of the
 chemically inactivated toxins and is designed to protect individuals
 against one or several related staphylococcal and streptococcal toxins.
 It is used for the diagnosis and treatment or amelioration of
 superantigen-associated bacterial infections.

Sequence 1837 BP; 632 A; 318 C; 249 G; 638 T; 0 other;

Query Match 99.08; Score 1832.2; DB 21; Length 1837;
 Best Local Similarity 99.8%; Pred. No. 2.7e-285;
 Matches 1834; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 15 TCATGTTGACAGCTTATCATCGATAAGCTTACTTTTCGAATCAGGCTCTATCCTTGAAC 74
 Db |||||||
 1 TCATGTTGACAGCTTATCATCGATAAGCTTACTTTTCGAATCAGGCTCTATCCTTGAAC 60

QY 75 AGGTGCAACATAGATTAGGCGATGAGATTACCAGACAACATATGAACGATATATCTAC 134
 Db |||||||

Db 61 AGTGCACATAGATTAGGCGATGAGATTACCAGACAACATATGAACGATATATCTAC 120
 QY 135 ATACGCAATCGGCAATTGATGACATTGGAATTAATTTCAATCAATTTGTTACTAACAA 194
 Db |||||||
 121 ATACGCAATCGGCAATTGATGACATTGGAATTAATTTCAATCAATTTGTTACTAACAA 180
 QY 195 CACTAGATTGACAACTAATTTCTCAACAAAGCTTTAATTTAAACAATTTCAAGTAACTCC 254
 Db |||||||
 181 CACTAGATTGACAACTAATTTCTCAACAAAGCTTTAATTTAAACAATTTCAAGTAACTCC 240
 QY 255 ACCAGCTCCATCAATGCTTACCGTAAGTAATCAATACTTACTAAACCTTTGTACATCAA 314
 Db |||||||
 241 ACCAGCTCCATCAATGCTTACCGTAAGTAATCAATACTTACTAAACCTTTGTACATCAA 300
 QY 315 GGTTTTTTCTTTTTGTTGTTTCATGAGTTACCATAACTTTCTATATATTATTTGACAACTAA 374
 Db |||||||
 301 GGTTTTTTCTTTTTGTTGTTTCATGAGTTACCATAACTTTCTATATATTATTTGACAACTAA 360
 QY 375 ATTGACAACCTCTCAATTAATTTTCTGCTACTCAAAAGTTTCTTCATTTGATATAGTCT 434
 Db |||||||
 361 ATTGACAACCTCTCAATTAATTTTCTGCTACTCAAAAGTTTCTTCATTTGATATAGTCT 420
 QY 435 AATTCCACCATCACTTCTCCACTCTCTCTACCGTCACAACTTCATCATCTCTCATCTTT 494
 Db |||||||
 421 AATTCCACCATCACTTCTCTCCACTCTCTCTACCGTCACAACTTCATCATCTCTCATCTTT 480
 QY 495 TCGTGTGTACACATCAATCAATATCTTTCCGTTTTTACGCACTATCGCTACTGTGCA 554
 Db |||||||
 481 TCGTGTGTACACATCAATCAATATCTTTCCGTTTTTACGCACTATCGCTACTGTGCA 540
 QY 555 CCTAAATATACCCCTTATCAATCGTCTTTTAAACTCATCTATATATAAATTTTAT 614
 Db |||||||
 541 CCTAAATATACCCCTTATCAATCGTCTTTTAAACTCATCTATATATAAATTTTAT 600
 QY 615 CCTCTACCTATCTATTCTGTAAGTAATTAATTTTAAATAATACAACTTTTATTTAT 674
 Db |||||||
 601 CCTCTACCTATCTATTCTGTAAGTAATTAATTTTAAATAATACAACTTTTATTTAT 660
 QY 675 AATAAATTAATAATAAGTTAATTTTAAATAATACAACTTTTATTTATTTATA 734
 Db |||||||
 661 AATAAATTAATAATAAGTTAATTTTAAATAATACAACTTTTATTTATTTATA 720
 QY 735 GTTAGCTATTTTTCATTTGTTAGTAATTAATTTGTTAGTAATTAATTAATTAATTAAT 794
 Db |||||||
 721 GTTAGCTATTTTTCATTTGTTAGTAATTAATTTGTTAGTAATTAATTAATTAATTAAT 780
 QY 795 AGGAGAACCCAGATATAAATGGAGGATATTAATGGAAACAAATAAAGTATTTGAAG 854
 Db |||||||
 781 AGGAGAACCCAGATATAAATGGAGGATATTAATGGAAACAAATAAAGTATTTGAAG 840
 QY 855 AAAATGGTATTTTGTGTTTGTAGTGACATTTCTTGACATAACAACTCTCGAAGAGGTATTT 914
 Db |||||||
 841 AAAATGGTATTTTGTGTTTGTAGTGACATTTCTTGACATAACAACTCTCGAAGAGGTATTT 900
 QY 915 GCTCAACAAGACCCCGATCCCAAGCACTTCCACAGATCTAGTTTATAGTTTAAACCTTCAA 974
 Db |||||||
 901 GCTCAACAAGACCCCGATCCCAAGCACTTCCACAGATCTAGTTTATAGTTTAAACCTTCAA 960
 QY 975 AATATATATTTTCTTTATGAGGCTGACCCCTGTTACTACAGAGATGTGAATCTGTTGAT 1034
 Db |||||||
 961 AATATATATTTTCTTTATGAGGCTGACCCCTGTTACTACAGAGATGTGAATCTGTTGAT 1020
 QY 1035 CAACCTTTATCTCACCATTAAATATATATATATATATATATATATATATATATATATAT 1094
 Db |||||||
 1021 CAACCTTAGATCTCAGGATTTAATATATATATATATATATATATATATATATATATAT 1080
 QY 1095 ACTGAACCTTAAGAACCAAGAGATGGCAACTTTTATTAAGGATTAAGGATTAAGGATTAAG 1154
 Db |||||||
 1081 ACTGAACCTTAAGAACCAAGAGATGGCAACTTTTATTAAGGATTAAGGATTAAGGATTAAG 1140
 QY 1155 GGCTGAGAAATATACCATCTCTGTTATTTATGTAATATGTAATATGTAATATGTAATATG 1214
 Db |||||||
 1141 GGCTGAGAAATATACCATCTCTGTTATTTATGTAATATGTAATATGTAATATGTAATATG 1200

QY 1215 TAGGAGGGGTAAACAATCATGAGGGGAATCATTTAGAAATTCCTAAAAAGATAGTCGTT 1274
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1201 TAGGAGGGGTAAACAATCATGAGGGGAATCATTTAGAAATTCCTAAAAAGATAGTCGTT 1260
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1275 AAAGTATCAATCGATGGTATCCAAAGCCTATCATTTGATTTGAAACAATAAAAAAATG 1334
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1261 AAAGTATCAATCGATGGTATCCAAAGCCTATCATTTGATTTGAAACAATAAAAAAATG 1320
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1335 GTAAGTCTCAAGAAATTAGACTATATAAGTTAGAAAATATCTTACAGATAATAAGCAACTA 1394
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1321 GTAAGTCTCAAGAAATTAGACTATATAAGTTAGAAAATATCTTACAGATAATAAGCAACTA 1380
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1395 TATACATAATGACCTCTCAATATGAAACTGGATATATAAGTTTACATACCTAAGAAATAA 1454
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1381 TATACATAATGACCTCTCAATATGAAACTGGATATATAAGTTTACATACCTAAGAAATAA 1440
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1455 GAAAGTTTTGGTTGATTTTTCCTGAAACCAAGATTTTACATCAATCAATATCTTATG 1514
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1441 GAAAGTTTTGGTTGATTTTTCCTGAAACCAAGATTTTACATCAATCAATATCTTATG 1500
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1515 ATATATAAGATAATGAAGCTTGACTCAACACAGCCAAATTTGAAGTCTACCTAACA 1574
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1501 ATATATAAGATAATGAAGCTTGACTCAACACAGCCAAATTTGAAGTCTACCTAACA 1560
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1575 ACCAAGTAACCTTTTGGCTTTGGCAACCTTACCTACTGCTGGATTTAGAAAATTTTATG 1634
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1561 ACCAAGTAACCTTTTGGCTTTGGCAACCTTACCTACTGCTGGATTTAGAAAATTTTATG 1620
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1635 AATTCCTTTTAAATGTAACCAAGCTGATTTGATGAGCGGTTTGTCTTATCTAAAGGA 1694
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1621 AATTCCTTTTAAATGTAACCAAGCTGATTTGATGAGCGGTTTGTCTTATCTAAAGGA 1680
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1695 GCTTTACCTCTTAATGCTGCAAAATTTTAAATGTTGATTTTGTATTTGCTATGCTAT 1754
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1681 GCTTTACCTCTTAATGCTGCAAAATTTTAAATGTTGATTTTGTATTTGCTATGCTAT 1740
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1755 TTGATGGTAAATCCCAATTTTTCGACAGACATCGTGGCGCACTCTTAACACCAAAATCAT 1814
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1741 TTGATGGTAAATCCCAATTTTTCGACAGACATCGTGGCGCACTCTTAACACCAAAATCAT 1800
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1815 AGACAGGAGCTTTAGCTTAGCAACTATTTTATCGTC 1851
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1801 AGACAGGAGCTTTAGCTTAGCAACTATTTTATCGTC 1837
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 6

ABN84229

ID ABN84229 standard; cDNA; 1837 BP.

XX AC ABN84229;

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PR 25-JUN-1997; 97US-0882431.

XX (USSA) US SEC OF ARMY.

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XX (USSA) US SEC OF ARMY.

XX Novel isolated and purified superantigen toxin DNA fragment which has been genetically altered, useful for producing vaccine for treatment of superantigen toxin-associated bacterial diseases

XX Disclosure; Column 61-63; 46pp; English.

XX The present sequence is the coding sequence of Streptococcus pyogenes vaccine SPEa42. The vaccine differs from the native SPEa sequence by substitution of the leu-42 residue by Arg. This mutation is expected to disrupt contact between the toxin and the HLA-DR receptor, reducing DRI binding. SPEa42 can be expressed as a recombinant protein in Escherichia coli as a secreted protein or as a cytoplasmic product. No indicators of toxicity have been detected for the purified recombinant protein, and vaccine studies demonstrate that SPEa42 is highly antigenic, inducing protective immunity in a mouse animal model. The attenuated superantigen can be used to protect against superantigen toxin infections. Methods of producing and using altered superantigen toxins as vaccines, and in diagnosis and therapy, are provided by the invention. A multivalent vaccine consisting of altered superantigen toxins from SEA, SEB, SEC-1, TST-1 and SPEa is predicted to provide protective immunity against the majority of bacterial superantigen toxins.

XX Sequence 1837 BP; 632 A; 318 C; 249 G; 638 T; 0 other;

Query Match 99.0%; Score 1832.2; DB 24; Length 1837;

Best Local Similarity 99.8%; Pred. No. 2.7e-285;

Matches 1834; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

15 TCATGTTGACAGCTTATCATCGATAGCTTACTTTTCGAATCAGGCTATCCTTGAAC 74

1 TCATGTTGACAGCTTATCATCGATAGCTTACTTTTCGAATCAGGCTATCCTTGAAC 60

75 AGTGCAACATAGATTAGGCGATGGAGATTACACAGCAACTATGAACGTATATATCTAC 134

61 AGTGCAACATAGATTAGGCGATGGAGATTACACAGCAACTATGAACGTATATATCTAC 120

135 ATACCGCAATCGCAATTTGATGACATTTGAACTAAATTCATCAATTTCTTACTACAAAG 194

121 ATACCGCAATCGCAATTTGATGACATTTGAACTAAATTCATCAATTTCTTACTACAAAG 180

195 CAATAGATTGACAACTAATTTCTCAACAAACGTTAATTTAAACAACATTCAGTAATCCC 254

181 CAATAGATTGACAACTAATTTCTCAACAAACGTTAATTTAAACAACATTCAGTAATCCC 240

255 ACCAGTCCATCAATGCTTACCGTAAGTAAATCAATCAATCAATCAATCAATCAATCAAT 314

241 ACCAGTCCATCAATGCTTACCGTAAGTAAATCAATCAATCAATCAATCAATCAATCAAT 300

315 GGTGTTTCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 374

301 GGTGTTTCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

375 ATTGACAACCTCTTCAATTTATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 434

361 ATTGACAACCTCTTCAATTTATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

435 AATTCCACCACATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 494

421 AATTCCACCACATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480

495 TCGTGTTGGTAAACACATATCAATATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 554

481 TCGTGTTGGTAAACACATATCAATATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540

QY	555	CTTAAATATACCCCTTATCAATCGCTCTTTAAACTCATCTATATATACATATTTTCAT	614	QY	1635	AATCTCTTTTATTAATGTAATAAACCGCTCATTTGATGAGCGGTTTTGCTTATCTAAAGGA	1694
Db	541	CTTAAATATACCCCTTATCAATCGCTCTTTAAACTCATCTATATATACATATTTTCAT	600	Db	1621	AATCTCTTTTATTAATGTAATAAACCGCTCATTTGATGAGCGGTTTTGCTTATCTAAAGGA	1680
QY	615	CTCTACCTATCTATTCGTAAAGAGATAAAATAAATACTATGTTTTTTTGTATTTTAT	674	QY	1695	GCTTTACCTCCCTAAATGCTGCAAAATTTTAAATGTTGGATTTTGTATTTGCTTATTTGAT	1754
Db	601	CTCTACCTATCTATTCGTAAAGAGATAAAATAAATACTATGTTTTTTTGTATTTTAT	660	Db	1681	GCTTTACCTCCCTAAATGCTGCAAAATTTTAAATGTTGGATTTTGTATTTGCTTATTTGAT	1740
QY	675	ATAAATATTAATATAGTAATGTTTTTTTAAATAATATACAAATTTTATCTATTTATA	734	QY	1755	TTGATGGGTAATCCCAATTTTCGACAGACATCGTCTGCACCTCTAAACACCAATCAT	1814
Db	661	ATAAATATTAATATAGTAATGTTTTTTTAAATAATATACAAATTTTATCTATTTATA	720	Db	1741	TTGATGGGTAATCCCAATTTTCGACAGACATCGTCTGCACCTCTAAACACCAATCAT	1800
QY	735	GTTAGCTATTTTTCATTTGTTAGTAATTTGTTGAATTTGTAATAACCTTTTAAATCTAG	794	QY	1815	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1851
Db	721	GTTAGCTATTTTTCATTTGTTAGTAATTTGTTGAATTTGTAATAACCTTTTAAATCTAG	780	Db	1801	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1837
QY	795	AGAGAACCCAGATATAAATGAGGAATTAATGGAACCAATTAATAAAGATTAATGAAG	854	RESULT 7			
Db	781	AGAGAACCCAGATATAAATGAGGAATTAATGGAACCAATTAATAAAGATTAATGAAG	840	AAH01002			
QY	855	AAATCGTATTTTCTGTTTGTAGTACATTTCTTGGACTAACATCTCGCAAGAGTATTT	914	ID	AAH01002	standard; DNA; 756 BP.	
Db	841	AAATCGTATTTTCTGTTTGTAGTACATTTCTTGGACTAACATCTCGCAAGAGTATTT	900	XX	AAH01002;		
QY	915	GCTCAACAGACCCGATCCAGCCAACTTCACAGATCTAGTTTGTATTTAAACCTTCAA	974	XX	24-JUL-2001	(first entry)	
Db	901	GCTCAACAGACCCGATCCAGCCAACTTCACAGATCTAGTTTGTATTTAAACCTTCAA	960	XX	Unidentified nucleotide sequence SEQ ID NO:993.		
QY	975	AATATATATTTCTTTATGAGGTGACCCCTGTTACTACAGAAATGTAATCTGTTGAT	1034	DE	Species specific; genus specific; family specific; probe: detection;		
Db	961	AATATATATTTCTTTATGAGGTGACCCCTGTTACTACAGAAATGTAATCTGTTGAT	1020	XX	Identification; algal; archaeal; bacterial; fungal; parasitological;		
QY	1035	CAACTTTTATCTCACCATTAAATATATATGTTTTCAGGGCCAAATATGATAAATFAAA	1094	KW	microorganism; diagnosis; translation elongation factor Tu; toxin;		
Db	1021	CAACTTTTATCTCACCATTAAATATATATGTTTTCAGGGCCAAATATGATAAATFAAA	1080	KW	translation elongation factor G; RecA recombinase; resistance;		
QY	1095	ACTGAACCTTAAGAACCAAGAGATGGCAACTTTATTTAAGGATAAAAACCTTGATTTAT	1154	KW	catalytic subunit of proton-translocating ATPase; antimicrobial;		
Db	1081	ACTGAACCTTAAGAACCAAGAGATGGCAACTTTATTTAAGGATAAAAACCTTGATTTAT	1140	XX	vaccine; primer; ds.		
QY	1155	GGTGTAGATATTTACCATCTCTGTTATTTATGTAAGAAATGCAGAAAGGAGTGCATGATC	1214	OS	Unidentified.		
Db	1141	GGTGTAGATATTTACCATCTCTGTTATTTATGTAAGAAATGCAGAAAGGAGTGCATGATC	1200	XX	WO200123604-A2.		
QY	1215	TACGGAGGGTAACAATCATGAAGGAATCATTTAGAAATTCCTAAAGAGATAGTCGTT	1274	XX	05-APR-2001.		
Db	1201	TACGGAGGGTAACAATCATGAAGGAATCATTTAGAAATTCCTAAAGAGATAGTCGTT	1260	XX	28-SEP-2000; 2000WO-CA01150.		
QY	1275	AAAGTATCAATCGATGATTCCTCAAGCCCTATCATTTTGATATTTGAAACAAATAAAAAATG	1334	XX	28-SEP-1999; 99CA-2283458.		
Db	1261	AAAGTATCAATCGATGATTCCTCAAGCCCTATCATTTTGATATTTGAAACAAATAAAAAATG	1320	PR	19-MAY-2000; 2000CA-2307010.		
QY	1335	GTAACCTGCTCAAGAAATAGACTATATAAGTTAGAAATATCTTACAGATATAAGCAACTA	1394	XX	(INFE-) INFECTIO DIAGNOSTIC (IDI) INC.		
Db	1321	GTAACCTGCTCAAGAAATAGACTATATAAGTTAGAAATATCTTACAGATATAAGCAACTA	1380	PA	Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;		
QY	1395	TATACTAATGACCTCTTAATATGAAGTGGATATATATAAGTTTCATACCTAAGATAAA	1454	PI	Picard FU, Roy PH;		
Db	1381	TATACTAATGACCTCTTAATATGAAGTGGATATATATAAGTTTCATACCTAAGATAAA	1440	XX	WPI; 2001-245006/25.		
QY	1455	GAAAGTTTTTGGTTGATTTTTTCCCTGACCAAGAAATTTACTCAATCTAAATATCTTATG	1514	XX	Nucleic acid sequences are used to generate universal probes and		
Db	1441	GAAAGTTTTTGGTTGATTTTTTCCCTGACCAAGAAATTTACTCAATCTAAATATCTTATG	1500	PT	primers which can be used to identify and detect the presence of algal,		
QY	1515	ATATATAAGATTAATGAAGCTTTGACTCAACACCAAGCAAAATGAAGTCTACCTAACCA	1574	PT	archaeal, bacterial, fungal and parasitological species in a test sample -		
Db	1501	ATATATAAGATTAATGAAGCTTTGACTCAACACCAAGCAAAATGAAGTCTACCTAACCA	1560	XX	Disclosure; Page 957; 1580pp; English.		
QY	1575	ACCAAGTAACCTTTTCTGTTTGGCAACCTTACCTACTGCTGGATTTAGAAATTTATTCG	1634	XX	The present invention describes a method for generating a repertory of		
Db	1561	ACCAAGTAACCTTTTCTGTTTGGCAACCTTACCTACTGCTGGATTTAGAAATTTATTCG	1620	CC	nucleic acids of tuf, fus, atpD and/or recA genes from which probes		
				CC	and/or primers are derived. The method comprises amplifying the nucleic		
				CC	acids of determined algal, archaeal, bacterial, fungal and parasitological		
				CC	species with a combination of defined primer pairs. The method can be		
				CC	used for producing probes and/or primers for detecting one or more		
				CC	related microorganisms e.g. algae, archaea, bacteria, fungi and		
				CC	parasites, for universal detection and for specific and ubiquitous		
				CC	detection and identification of an algal, archaeal, bacterial, fungal		
				CC	and parasitological species, genus, family and group. A nucleic acid (I)		
				CC	obtained using the method of the invention can be used for the universal		
				CC	detection of any bacterium, fungus or parasite in a sample and for the		
				CC	detection of at least one antimicrobial agent resistance gene or at		
				CC	least one toxin gene. hexA nucleic acids are used for the specific and		
				CC	ubiquitous detection and for identification of Streptococcus pneumoniae.		

Db 89 TTTAAAGCATACTTAATAATAAATAACATGAGATTATTAATAATAAATTAAGTTTC 148
QY 741 TATTTTTCATCTGTAGTAATCTGTAATCTTAATAACCTTTTAAATCTAGAGAGA 800
Db 149 TTTTAATGTTTTTTTAAATGAATTAATAGATTATACATATATTTAAAGTGTATCTAGA 208
QY 801 ACCAGATATAAA--ATGGAGGAATATTAAATGGAACAACAATAAAAGATTATGAAGAAA 858
Db 209 TACTTTTGGGAATGTTGGATAAAGAGAGATAAAAAATGATAAGAGATTATTTATTTTAC 268
QY 859 TGGTATTTTGTGTTTT--AGTGACATTTCTTGGACTAACATCTCGCAAGAGGTATTG 915
Db 269 ATGTAATTTTGATATTCGCACTGATATTAGTTATTTCTACACCAACGTTTATAGCAGAGA 328
QY 916 CTCACAAGACCCGATCAAGCAACTTCACAGATCTAGTTAGTTAA---AAACCTTC 972
Db 329 GTCAACAGATCTTAACACAGATGAGTTGCACAAATCGAGTAATTCACCTGTTGATGG 388
QY 973 AAAATATATATTTCTTTATGAGGGTGACCCCTTACTCACGAGAATGGAATCTGTTG 1032
Db 389 AAGATATGAAGTTTGTATGATGATAATCATGTATCAGCAATAAAGCTTAATATCTATAG 448
1033 ATCAACTTTTATCTCACCATTAAATATATAATGTTTTCAGGGCAA-----ATTATG 1083
Db 449 ATCAATTTCTATCTTGTACTTAAATATATTTCTAATAGGACACTAAGTTAGGGGATTATG 508
QY 1084 ATAAATTAATAAAGTAAAGTAAAGCAAGAGATGCAACTTTTATTAAGGATAAAAAACG 1143
Db 509 ATAATCTCGAGTCGAATTTAAACCAAGATTAGCTGATATAATACAAAGATAAATACG 568
QY 1144 TTGATATTTATGTTGTAAGATATATACCATCTCTGTTTATTATGTGAAA-----1192
Db 569 TAGATCTGTTGGAGCTAATATATATTTATTAATCAATGTTATTTCTAATAAAGCAAGATGATA 628
QY 1193 -----TGCAGAAAGAGTGCATGTATCTACGAGGGGTAACAAATCATG 1236
Db 629 TTAATTCGATCAAACTGACAAACGAAACCTTGTATGTATGGTGTAACTGACGATA 688
QY 1237 AAGGGAATCATTTAGAAATTCCTTAAAGATAGTCGTTAAAGTATCAATCGATGGATCC 1296
Db 689 ATGGAACCAATFAGATAAATAFAGAATATTACTGTCGGGTATTGGAAGTGGTAAAA 748
QY 1297 AAGCCATCATTTGATATGAACAATAAATAAATGTTAACTGCTCAAGAAATAGACT 1356
Db 749 ATTTATATCTTTTGGACGACAACTAATAAGAAAAAGGTGACTGCTCAGAATTAGATT 808
QY 1357 ATAAAGTTAGAAATATCTACAGATAATAAGCACTATATCTAATGAGCCTTCTAAAT 1416
Db 809 ACCTAATCGTCACTATTTGGTGAAAATATAAATACTATGAAATTAACAACCTCGCCTT 868
1417 ATGAAACTGGATATATAAGTTTCATACCTAAGAAATAAAGAAAGTTTTTGGTTGATTTTT 1476
Db 869 ATGAAACGGGATATATAAATTTATA--GAAATGAGAATAGCTTTTGTATGACATGA 925
QY 1477 TCCTCAACAG-----AATTTACATCAATTAATATCTTATGATATATAAAGATAATG 1530
Db 926 TGCCCTCCACGAGAGATAAATTTGCCCAATCTAAATATTTAATGATGTACAAATGACAATA 985
QY 1531 AAACGCTTGACTCAACACACAGCAAAATGCACTACCTTAACCAACCAAGTAA 1583
Db 986 AATGTTGATCTTAAGATGTGAAGTTGAAGTTTATCTTACGACCAAGAAA 1038

RESULT 9

ABN84224

ID ABN84224 standard; cDNA; 1712 BP.

XX AC ABN84224;

XX DT 23-SEP-2002 (first entry)

XX ST Staphylococcal enterotoxin B vaccine (B42360210).

XX

KW

Enterotoxin B; superantigen; antigen; toxin; vaccine; B42360210;

attenuation; mutant; gene; ss.

Staphylococcus sp.

Key Location/Qualifiers

CDS 244..1044

/*tag= a

/product= "SEB vaccine"

XX

US6399332-B1.

XX

04-JUN-2002.

XX

01-SEP-1998; 98US-0144776.

XX

25-JUN-1997; 97US-0882431.

XX

(USSA) US SEC OF ARMY.

XX

Ulrich RG, Olson MA, Bavari S;

XX

WPI; 2002-546281/58.

XX

P-PSDB; ABB79503.

XX

Novel isolated and purified superantigen toxin DNA fragment which has

been genetically altered, useful for producing vaccine for treatment of

superantigen toxin-associated bacterial diseases

XX

Disclosure; Column 39-41; 46pp; English.

XX

The present sequence is the coding sequence of staphylococcal

enterotoxin B (SEB) vaccine B42360210. The invention relates to a

vaccine against superantigen toxin-associated bacterial diseases.

Superantigen vaccines were developed by engineering changes in the

receptor-binding portions of superantigen toxins such as SEB to

reduce receptor-binding affinities and toxicity while maintaining

antigenicity. In examples from the invention, attenuated

superantigen toxins were shown to protect animals against challenge

with wild-type toxin. Methods of producing and using the altered

superantigen toxins as vaccines, and in diagnosis and therapy, are

provided. A multivalent vaccine consisting of altered superantigen

toxins from SEA, SEB, SEC-1, TSSP-1 and streptococcal SpeA is

predicted to provide protective immunity against the majority of

bacterial superantigen toxins.

XX

SQ Sequence 1712 BP; 596 A; 223 C; 255 G; 638 T; 0 other;

QY

Query Match 10.0%; Score 184.2; DB 24; Length 1712;

Best Local Similarity 54.5%; Pred. No. 6.3e-21;

Matches 552; Conservative 0; Mismatches 408; Indels 53; Gaps 7;

Db 621 ACCTATCTATTCGTATAAAGATAAATAAATACTATGTTTGTGTTATTTAATAAAA 680

QY 29 AACACTATGTTGTTAAAGATGTTTTCGTATATAAGTTAGTGTAGTACTACTTAAT 88

Db 681 ATTATTAATAAAGTAAATCTTTTAAAAATATACAAATTTATCTATTATAGTTAGC 740

QY 89 TTTAAAAGCATACTTAATTAATAATAACATGAGATTAATAAATATATTAAGTTTC 148

Db 741 TATTTTTCATGTTAGTAAATATGGTGAATGTTGAATAACTTTTAAATCTAGAGAGA 800

QY 149 TTTTAATGTTTTTTTAAATGAAATTAAGATTAATAATATATTAAGTGTATCTAGA 208

Db 801 ACCAGATATAAA--ATGGAGGATATTAATGGAACAATAAATAAAGTATGGAAGAA 858

QY 209 TACTTTTGGGAATGTTGGATAAAGGAGATAAAAAATGTAAGAGATTATTTATTCAC 268

Db 859 TGGTATTTTGTGTTTT--AGTGACATTTCTTGGACTTAACAATCTCGCAAGAGATTG 915

QY 269 ATGTAATTTTGATATTCGCACTGATATAGTTATTTCTACACCAAGCTTTACAGAGA 328

Db 916 CTCAACAAGACCCCGATCCAAAGCCAACTTCACAGATCTAGTTAGTTAA---AAACCTTC 972

QY


```

Db      323  ATAAATTTAGGGCACATGATTTTAAATTTATAACATTTAGTGATAAAAACTGAAAAATTTATG 382
Qy      1084  ATAAATTTAAACTGAACTTTAAGAACCAAGAGATGGCAACTTTATTAAAGGATAAAAAACG 1143
Db      383  ACAAGTCAAAACAGAGTTATTAAATGAAGGTTAGCAAGAGATGACAAAGATGAAGTAG 442
Qy      1144  TTGATATTTATGGTGTAGAATATTACCATCTCTGTTATTAT----- 1185
Db      443  TTGATGTGTATGGATCAATTTACTATGTAAACTGCTATTTTCATCCAAAGATAATGTAG 502
Qy      1186  GTGAAATGCAGAAAGAGTGCATGTATCTACGGAGGGTAACAAATCATCAGAGGAATC 1245
Db      503  GTAAAGTTACAGTGGCAAACTTGTATGTATGGAGGATAACAAAAACATCAAGGAACC 562
Qy      1246  ATTTAGAAATTCCTA-----AAAAGATACCTGTTAAAGTATCAATCGATGGTATCCAAA 1299
Db      563  ACTTTGATAATGGGAACCTTACAAATGTACTTTATAGAGTTTATGAAAAATAAAGAAACA 622
Qy      1300  GCCTATCATTGTATTTGAACAAATAAAAAAATGGTAACTGCTCAAGAAATTAGACTATA 1359
b      623  CAATTTCTTTTGAAGTCAAACTGATAAGAAAGTGTAAACAGCTCAAGAACTAGACATAA 682
Qy      1360  AAGTTAGAAATATCTTACAGATAAATAAGCAACTATATACTAATGGACCTTCTAAATATG 1419
Db      683  AAGCTAGGAATTTTAAATTAATAAAAAAATTTGTATGAGTTTAAACAGTTCCACCATATG 742
Qy      1420  AAACGTGATATATAAGTTTCATACCTAAGATAAAGAAAGTTTTGGTTTGAATTTTCC 1479
Db      743  AAACAGGATATATAAATTTATTGAAATAAACGGCAATCTTTTGGTATGATATGATGC 802
Qy      1480  CTGAACCG-----AATTTACTCAATCTAAATATCTTATGATATATAAAGATAATGAAA 1533
Db      803  CTGCACCGCGGATAAGTTTGACCAATCTAAATATTTAATGATGTACACGACAATAAAA 862
Qy      1534  CGCTTGACTCAACACAGCCAAATTTGAAGTCTACCTTAAACCAAGTA 1582
Db      863  CGGTTGATCTAAAGTGTGAAGATAGAGTCCACCTTACAACAAAGAA 911
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Search completed: August 21, 2003, 06:35:13
Job time : 625 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 21, 2003, 12:20:34 ; Search time 36 Seconds
(without alignments)
670.509 Million cell updates/sec

Title: US-09-308-830A-13
Perfect score: 1323
Sequence: 1 MNNKKVKKMKVFFVLVTF.....KDNETLDSNTSQIEVYLTK 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1314	99.3	251	1 S29659	exotoxin type A pr
2	1238	93.6	236	2 S18783	exotoxin type A pr
3	1233	93.2	236	2 S18786	exotoxin type A pr
4	1108	83.7	236	2 S18789	exotoxin A precurs
5	1074.5	81.2	250	1 A26152	streptococcal pyro
6	575.5	43.5	266	1 ENSAB6	enterotoxin B prec
7	550.5	41.6	266	2 S11885	enterotoxin C3 - S
8	548	41.4	266	2 A60114	enterotoxin C-2 pr
9	547	41.3	266	1 ENSAC1	enterotoxin C-1 pr
10	480	36.3	258	2 G89968	extracellular ente
11	345	26.1	258	2 A33953	enterotoxin D prec
12	341	25.8	260	2 C89984	enterotoxin P (imp
13	337	25.5	260	2 A89969	enterotoxin YEN2
14	337	25.5	260	2 E89969	enterotoxin Sen [i
15	316.5	23.9	258	2 H89968	enterotoxin Sen [i
16	313	23.7	257	2 A28179	enterotoxin E prec
17	312	23.6	257	2 A28179	enterotoxin A prec
18	304.5	23.0	240	2 G89991	extracellular ente
19	270	20.4	239	2 D89969	enterotoxin SEM [i
20	245.5	18.6	242	2 C89969	extracellular ente
21	210	15.9	235	2 A30509	exotoxin C precurs
22	173	13.1	133	2 B89969	enterotoxin Yent1
23	129.5	9.8	231	2 D89807	exotoxin 11 [impor
24	127	9.6	157	2 A89942	hypothetical prote
25	125	9.4	227	2 C89808	exotoxin 15 [impor
26	118	8.9	234	2 C89992	toxic shock syndro
27	117.5	8.9	234	2 C89807	exotoxin 10 [impor
28	116	8.8	234	1 XCSAS1	toxic shock syndro
29	114	8.6	292	2 B89807	exotoxin 9 [import

30	112	8.5	232	2 F89807	exotoxin 13 [impor
31	110.5	8.4	231	2 H89806	exotoxin 7 [impor
32	109.5	8.3	1367	2 T18456	hypothetical prote
33	106.5	8.0	241	2 B89888	hypothetical prote
34	106	8.0	434	2 T28342	ORF MSV181 hypothe
35	105.5	8.0	596	2 E96935	FUSION, methionine
36	105.5	8.0	825	2 C89888	hypothetical prote
37	104.5	7.9	241	2 C89888	hypothetical prote
38	103.5	7.8	1306	2 T28313	ORF MSV152 probabl
39	103.5	7.8	1856	2 C95008	immunoglobulin Al
40	103	7.8	235	2 C97252	probable membrane
41	102.5	7.7	768	2 D71726	outer membrane pro
42	102.5	7.7	1790	2 S67593	transport protein
43	101.5	7.7	518	2 G70174	hypothetical prote
44	101	7.6	387	2 E82881	hypothetical prote
45	101	7.6	770	2 B48910	desmocollin 1b pre

ALIGNMENTS

RESULT 1

S29659

exotoxin type A precursor (allele 1) - Streptococcus pyogenes phage T12
N:Alternate names: erythrogenic toxin; scarlet fever toxin

C:Species: Streptococcus pyogenes phage T12

C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 10-Sep-1999

C:Accession: S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800

R:Weeks, C.R.; Ferretti, J.J.

Infect. Immun. 52, 144-150, 1986

A:Title: Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin

A:Reference number: S29659; MUID:86166804; PMID:3514452

A:Accession: S29659

A:Molecule type: DNA

A:Residues: 1-251 <WEB>

A:Cross-references: GB:040453; EMBL:M19350; NID:gl877426; PIDN:AAC48868.1; PID:gl8774

R:Nelson, R.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.

J. Exp. Med. 174, 1271-1274, 1991

A:Title: Characterization and clonal distribution of four alleles of the speA gene en

A:Reference number: S18782; MUID:92044323; PMID:1940804

A:Accession: S18782

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 9-244 <NEA>

A:Cross-references: EMBL:X61560; NID:g47287; PIDN:CAA43758.1; PID:g47288

A:Experimental source: Streptococcus pyogenes strain MGAS156 isolate Nebraska unassign

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199

A:Accession: S18784

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 9-244 <NEA>

A:Cross-references: EMBL:X61556; NID:g47291; PIDN:CAA43754.1; PID:g47292

A:Experimental source: Streptococcus pyogenes strain MGAS165 isolate Minnesota unassign

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199

A:Accession: S18785

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 9-244 <NEZ>

A:Cross-references: EMBL:X61559; NID:g47293; PIDN:CAA43757.1; PID:g47294

A:Experimental source: Streptococcus pyogenes strain MGAS167 isolate Texas unassigned

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199

A:Accession: S18791

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 9-244 <NEY>

A:Cross-references: EMBL:X61555; NID:g47309; PIDN:CAA43753.1; PID:g47310

A:Experimental source: Streptococcus pyogenes strain MGAS327 isolate Arizona unassign

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199

A:Accession: S18796

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 9-244 <NEO>

A:Cross-references: EMBL:X61557; NID:g47319; PIDN:CAA43755.1; PID:g47320

A>Note: the nucleotide sequence was submitted to the EMBL Data Library.
A:Accession: S18794
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NE>
A:Cross-references: EMBL:X61570; NID:q47315; PIDN:CAAA43768.1; PID:q47316
A:Experimental source: strain MGAS491 isolate United Kingdom unassigned
A>Note: the nucleotide sequence was submitted to the EMBL Data Library.
A:Accession: S18801
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NE>
A:Cross-references: EMBL:X61572; NID:q47333; PIDN:CAAA3770.1; PID:q47334
A:Experimental source: strain MGAS524 isolate Germany unassigned phage
A>Note: the nucleotide sequence was submitted to the EMBL Data Library.
A:Accession: S18798
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NE>
A:Cross-references: EMBL:X61571; NID:q47323; PIDN:CAAA3769.1; PID:q47324
A:Experimental source: strain MGAS495 isolate Germany unassigned phage
A>Note: the nucleotide sequence was submitted to the EMBL Data Library.

```
C;Genetics:
```

```
A;Gene: A0A0P7C968
```

```
C;Superfamily: enterotoxin B
```

```
C;Keywords: exotoxin
```

```
F;1-22/Domain: signal sequence predicted <SIG>
```

```
F;23-236/Product: exotoxin type A (fragment) #status predicted <MAT>
```

```
Query Match          93.6%; Score 1238; DB 2; Length 236;
```

```
Best Local Similarity 99.2%; Pred. No. 1.2e-85;
```

```
Matches 234; Conservative 1; Mismatches 1; Indels 0; Gaps 0
```

```
QY      9 KKMVFVLVTFGLTISOEVAQQDDPSQLHRSLSVKLNQNIVFLYEGGDPVTHENVKK  
| | | |  
Db       1 KKMVFVLVTFGLTISOEVAQQDDPSQLHRSLSVKLNQNIVFLYEGGDPVTHENVKK  
| | | |  
QY     69 DOLLSHLLIYNYSGPNYDKLTTELKNQMATLFDKKNVDIYGVEYYHLCYLCENAEKS  
| | | |  
Db     61 DQLSLDILLIYNYSGPNYDKLTTELKNQMATLFDKKNIDVIYGVEYYHLCYLCENAEKS  
| | | |  
QY    129 IYGVGTNHSGHNLETPPKKIIVKVVSIDGTQSISFDETNNKKMVMTAQEILDYKVRKYLTDN  
| | | |  
Db    121 IYGVGTNHSGHNLETPPKKIIVKVVSIDGTQSISFDETNNKKMVMTAQEILDYKVRKYLTDN  
| | | |  
OY   189 LYTGNSPKYTGYIKFIPIKNKESFWFFDFPEPETOSKILMIYADNETLDNSTSQI 2
```

161 LTINGFSKIEUIG.IRAIFANNESFWDFPFEPETIQSKLEMLIKNDALILDSN15Q1

RESULT 3
S18786

extotoxin type A precursor (allele 2) - Streptococcus pyogenes phage (str N;Alternate names: scarlet fever toxin
C;Species: Streptococcus pyogenes
A;Variety: Streptococcus pyogenes California; strain MGAS251 isolate Cal
A;Accession: S18786
C;Date: 29-Jan-1993 #sequence revision 29-Jan-1993 #text change 16-Jul-1
C;Accession: S18786; S18787; S18788; S18790; S18792; S18795; S18799
R;Nelson, K.; Schlievert, P.M.; Sclander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A;Title: Characterization and clonal distribution of four alleles of the
A;Reference number: S18783; MUID:92044323; PMID:1940804
A;Accession: S18786
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NBL>
A;Cross-references: EMBL:X61561; NID:q47297; PIDN:CAA43759.1; PID:q47298
A;Experimental source: strain MGAS250 isolate California unassigned phag
A;Note: the nucleotide sequence was submitted to the EMBL Data Library,
A;Accession: S18787
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

A:Residues: 1-236 <NEA>
A:CROSS-references: EMBL:X61562; NID:g47299; PIDN:CAA43760.1; PID:g47300
A:Experimental source: strain MGAS251 isolate California unassigned phase
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18788
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEA>
A:CROSS-references: EMBL:X61563; NID:g47301; PIDN:CAA43761.1; PID:g47302
A:Experimental source: strain MGAS256 isolate California unassigned phase
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18790
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEA>
A:CROSS-references: EMBL:X61564; NID:g47305; PIDN:CAA43762.1; PID:g47306
A:Experimental source: strain MGAS285 isolate Colorado unassigned phase
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18792
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEA>
A:CROSS-references: EMBL:X61565; NID:g47311; PIDN:CAA43763.1; PID:g47312
A:Experimental source: strain MGAS480 isolate Yugoslavia unassigned phase
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18795
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEA>
A:CROSS-references: EMBL:X61566; NID:g47317; PIDN:CAA43764.1; PID:g47318
A:Experimental source: strain MGAS492 isolate United Kingdom unassigned phase
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18799
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEA>
A:CROSS-references: EMBL:X61567; NID:g47325; PIDN:CAA43765.1; PID:g47326
A:Experimental source: strain MGAS496 isolate Germany unassigned phase
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C:Genetics:
A:Gene: speA2
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F:23-236/Product: exotoxin type A (fragment) #status predicted <MAT>

Query Match 93.2%; Score 1233; DB 2; Length 236;
Best Local Similarity 99.2%; Pred. No. 2.9e-85;
Matches 234; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 KKMVFVLTFLGLTISQEVFAQQDPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 68
DB 1 KKMVFVLTFLGLTISQEVFAQQDPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 60

QY 69 DQLSHLLIYVSGPNYDKLTKELKNQEMATLFKDKNVDIYGVYYHLCYLCEAERSAC 128
DB 61 DQLSHLLIYVSGPNYDKLTKELKNQEMATLFKDKNVDIYGVYYHLCYLCEAERSAC 120

QY 129 IYGVVTHNHEGNHLEIPKPIVWVSVSDIGIQLSFDIETNKKMVTQAQELDYKVRKYLTDNQ 188
DB 121 IYGVVTHNHEGNHLEIPKPIVWVSVSDIGIQLSFDIETNKKMVTQAQELDYKVRKYLTDNQ 180

QY 189 LYTNGPSKYETGYIKFIPKNKESFWDFPEPEFTOSKYLMIYKDNETLDSNTSQI 244
DB 181 LYTNGPSKYETGYIKFIPKNKESFWDFPEPEFTOSKYLMIYKDNETLDSNTSQI 236

RESULT 4
S18789
exotoxin A precursor (allele 4) - Streptococcus pyogenes (strain MGAS262 isolate California
N:Alternate names: scarlet fever toxin
C:Species: Streptococcus pyogenes
A:Variety: strain MGAS262 isolate California

C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C:Accession: S18789
C:Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A:Title: Characterization and clonal distribution of four alleles of the speA gene
A:Reference number: S18782; MUID:92044323; PMID:1940804
A:Accession: S18789
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEL>
A:CROSS-references: EMBL:X61573; NID:g47303; PIDN:CAA43771.1; PID:g47304
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C:Genetics:
A:Gene: speA
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F:23-236/Product: exotoxin A (fragment) #status predicted <MAT>

Query Match 83.7%; Score 1108; DB 2; Length 236;
Best Local Similarity 88.6%; Pred. No. 6.7e-76;
Matches 209; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 9 KKMVFVLTFLGLTISQEVFAQQDPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 68
DB 1 KKMVFVLTFLGLTISQEVFAQQDPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 60

QY 69 DQLSHLLIYVSGPNYDKLTKELKNQEMATLFKDKNVDIYGVYYHLCYLCEAERSAC 128
DB 61 DQLSHLLIYVSGPNYDKLTKELKNQEMATLFKDKNVDIYGVYYHLCYLCEAERSAC 120

QY 129 IYGVVTHNHEGNHLEIPKPIVWVSVSDIGIQLSFDIETNKKMVTQAQELDYKVRKYLTDNQ 188
DB 121 IYGVVTHNHEGNHLEIPKPIVWVSVSDIGIQLSFDIETNKKMVTQAQELDYKVRKYLTDNQ 180

QY 189 LYTNGPSKYETGYIKFIPKNKESFWDFPEPEFTOSKYLMIYKDNETLDSNTSQI 244
DB 181 LYTNGPSKYETGYIKFIPKNKESFWDFPEPEFTOSKYLMIYKDNETLDSNTSQI 236

RESULT 5
A26152
streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.
N:Alternate names: scarlet fever toxin; SPE type A (speA)
C:Species: Streptococcus sp.
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A26152
R:Johnson, L.P.; L'Italien, J.J.; Schlievert, P.M.
Mol. Gen. Genet. 203, 354-356, 1986
A:Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to
A:Reference number: A26152; MUID:86284313; PMID:3526093
A:Accession: A26152
A:Molecule type: DNA
A:Residues: 1-250 <JOH>
C:Superfamily: enterotoxin B
C:Keywords: exotoxin

Query Match 81.2%; Score 1074.5; DB 1; Length 250;
Best Local Similarity 83.7%; Pred. No. 2.3e-73;
Matches 210; Conservative 7; Mismatches 33; Indels 1; Gaps 1;

QY 1 MENNKVKKMVFVLTFLGLTISQEVFAQQDPDSQLHRSSLVKNLQNIYFLYEGDPV 60
DB 1 MENNKVKKMVFVLTFLGLTISQEVFAQQDPDSQLHRSSLVKNLQNIYFLYEGDPV 60

QY 61 THENKVSVDQLSHLLIYVSGPNYDKLTKELKNQEMATLFKDKNVDIYGVYYHLCYLCE 120
DB 61 THENKVSVDQLSHLLIYVSGPNYDKLTKELKNQEMATLFKDKNVDIYGVYYHLCYLCE 120

QY 121 ENAERSACIYGGVTHNHEGNHLEIPKPIVWVSVSDIGIQLSFDIETNKKMVTQAQELDYKVR 180
DB 121 ENAERSACIYGGVTHNHEGNHLEIPKPIVWVSVSDIGIQLSFDIETNKKMVTQAQELDYKVR 179

Qy	181	KYLTDNKQYLITNGPSKYETGYIKFIPKKNKSEFWDFPEPEFTQSKYLYMYKONETLDSN	240
Db	180	KYLTDNKQYLITNGPSKYETGYIKFIPKKNKSEFWDFPEPEFTQSKYLYMYKONETLDSN	239
Qy	241	TSQIEVYLTTK	251
Db	240	TSQIEVYLTTK	250

RESULT 6
ENSAB6
enterotoxin B precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 24-Apr-1984 #sequence_revision 15-Oct-1996 #text_change 18-Jun-1999
C:Accession: S27360; A92065; S27240; A01815
R:Jones, C.L.; Khan S.A.
J. Bacteriol. 166, 29-33, 1986
A:Title: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.
A:Reference number: S27360; MUID:86168029; PMID:3957869

A: Molecule type: DNA
A: Residues: 1-266 <TON>
A: Cross-references: EMBL:M1118; NID:g152999; PIDN:AAA8550.1; PID:g153000
A: Experimental source: strain S6
R: Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3518-3525, 1970
A: Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromide
A: Reference number: A92065; MUID:71007902; PMID:5470821
A: Accession: A92065

A: Molecule type: protein
A: Residues: 28-55, 'ND', 59-68, 'NE', 71, 'FDLYLV', 78-117, 119-127, 'N', 129, 'D', 131-132, 'ENT',
A: Experimental source: strain S-6
R: Huang, I. Y.; Bergdoll, M. S.
J. Biol. Chem. 245, 3511-3517, 1970
A: Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, composition
A: Reference number: A92064; MUID:71007901; PMID:5470820
A: Contents: annotation; chymotryptic peptides
R: Huang, I. Y.; Bergdoll, M. S.
J. Biol. Chem. 245, 3493-3510, 1970
A: Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, composition
A: Reference number: A92063; MUID:71007900; PMID:5470819
A: Contents: annotation; tryptic peptides
R: Schantz, E. J.; Roessler, W. G.; Wagman, J.; Spero, L.; Dunnerv. D. A.; Beradoll, M. S.

Biochemistry 4, 1011-1016, 1965

A;Title: Purification of staphylococcal enterotoxin B.
A;Reference number: A90548; PMID:66035792; PMID:4953912
A;Contacts: annotation; biological source of protein
R;Alakhov, V.Y.; Klinsky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.; Moskaleva, E.Y.; Sveshin,
Eur. J. Biochem. 209, 823-828, 1992
B;Title: Identification of functionally active fragments of staphylococcal enterotoxin B
A;Reference number: S27240; PMID:93049338; PMID:1425690
A;Accession: S27240
A:Molecule type: protein
A;Residues: 28-42;128-148 <ALA>
C;Superfamily: enterotoxin B
F;i-27/Domain: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin B #status experimental F<MAT>
F;120-140/Disulfide bonds: #status experimental

Query Match 43.5%; Score 575.5; DB 1; Length 266;
Best Local Similarity 48.2%; Pred. No. 6.2e-36;
Matches 123; Conservative 38; Mismatches 75; Indels 19; Gaps 7;

15	QY	VLVTFGLTIS-QEVEA--QODPPSQSLHSSLVKNI-QNIYFLYBGDPVTHENVKSDQ	70
		: :	
11	Db	ILIFALLIVITPNVLAESQDPKPRDELHKSSFTGLMENMKVLVDNHNVSAINKYSIDQ	70
		: :	
71	QY	LISHHLIYVSGP---NYDKLKYELKNOEMATLFDKKNVDIYGEVYHILCYLCEA----	123
		: :	
71	Db	FLYFDLIYSIKDTKLGNVDNRVEFNKDLADKYKDYVDFGANGYIYOCYFSKKTNDIN	130
		: :	
124	QY	-----ERSACTIYGGVTNHEGNHLEIPKKIYKVSIDIGISLSLFDIETNKKWTAQELDYK	178

[illegible]

RESULT 7
S11885
enterotoxin C3 - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1997
C:Accession: S11885
R:HoVde, C.J.; Hackett, S.P.; Bohach, G.A.
Mol. Gen. Genet. 220, 329-333, 1990
A:Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
A:Reference number: S11885; MUID:90220508; PMID:2325627
A:Accession: S11885
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-266 <HOV>
A:Cross-references: GB:X51661; NID:g46570; PIDN:CAA35972.1; PID:g46571
C:Superfamily: enterotoxin B

```

Query Match      41.68; Score 550.5; DB 2; Length 266;
Best Local Similarity 46.18; Pred. No. 4.7e-34;
Matches 117; Conservative 46; Mismatches 74; Indels 17; Ga

Qy 15 VLVTFLGLTIS-OEVFAQDDP--PSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKYS
Db 11 ILIFALLIVISTPNVLAESQDPMPDDLHKSSFEETCTGMNKMKYLDYDHYVSATKYKS
Qy 71 LLSHLLIYNVSG---PNYDKLTAKLNQEMATFLPKDNVDYDYGVEYHYLCYC--EN
Db 71 FLAHLIYNISDKKLNKYKVTLELNEDLAKKYKDEVVDYGVSNYVNCYFSSKDN
Qy 126 ----SACIYGGVYNHEGNHLEIP--KKIVKVSIDIGISLFIETNKKWVAQAEILD
Db 131 VTGGKTCMYGIGTKHEGNHFDNGNLQNLVLRVRYENKRNITISEVQTDKKSVTAQAEILD
Qy 180 RXYLTDNKOLYTNGPSKYETGYTKFTPKKNESFWDFFPBP--EFTQSKYLIYMYKDN
Db 191 RNLINKNNKYENSSPYETGYTKFIENNGNTFWYDMMPAPGDKFDQSKYLLMYNDN
Qy 238 DSNTSQIEVYLTTK 251
Db 251 DSKSVKIEVHLTK 264

```

```

RESULT 8
A601114
enterotoxin C-2 precursor - Staphylococcus aureus
N:Alternate names: enterotoxin C-3 precursor.
C:Species: Staphylococcus aureus
C:Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 16-Jul-
C:Accession: A60114; B60114; A33866
R:Bohach, G.A.; Schlievert, P.M.
Infect. Immun. 57, 2249-2252, 1989
A:Title: Conservation of the biologically active portions of staphyloco
A:Reference number: A60114; MUID:89277549; PMID:2543637
A:Accession: A60114
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-266 <BOH>
A:Accession: B60114
A:Molecule type: protein
A:Residues: 28-66 <BOH2>
R:Couch, J.L.; Betley, M.J.

```



```

Db      12  LIFALLVLYFTNVLAEE---SQPDPTFDELHKASKFTGLMENKNKVLVDHRYVSATKVKSV 68
      QY      69  DOLLSHHLIYNSYG---PNVDKLTKEKNOEMATLFKDKNVDIYGYEYHLCVLC--ENA 123
      Db      69  DFLAHDLIYNTSDKKLKNYDKVKTLELLEGLAKKYDEVDVYGSYNYVNCYFSSKDNV 128
      QY      124  ER----SACIYGGVTNHGHNHLEIP--KKIVVKVSDIGQSLSFDIETNKKMVTQAQELDY 177
      Db      129  GKVGTGKTCMYGGITKHEGHNHFDGNLQNVLRVYENKRNITISFEVTDKSKSVTAQELDI 188
      QY      178  KVKRYLTDNKQLYTNGPSKYETGYIKFIPKPKNESFWDFPEP--EFTQSKYLMYKDN 235
      Db      189  KARNFTLINKNLYEFNSSPYETGYIKFIENNGNTFWYDMPAPGDKFDSQSKYLLMYNDNK 248
      QY      236  TLDSTNTSQIEVILYTTK 251
      Db      249  TVDSKSVKIEVHLTTK 264

RESULT 10
G89968
extracellular enterotoxin type G precursor [imported] - Staphylococcus aureus (strain
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: G89968
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O-
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.
C: Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G89968
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <R>
A:A:Cross-references: GB:BA000018; PID:g13701617; PIDN:BAB42910.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: seg
C:Superfamily: enterotoxin B

Query Match 36.3%; Score 480; DB 2; Length 258;
Best Local Similarity 40.7%; Pred. No. 8.6e-29;
Matches 105; Conservative 46; Mismatches 91; Indels 16; Gaps 5;

QY      8  LKKMWFVLVTFGLTISQEVFAQQDDP--SQLHRSSLVKN----LQNTIFYLEGDPVT 61
Db      1  MKKLSTVITLILIEIVFHNMYNAQPDPKLDELNKVSDYKKNKGTMGNYMNYLTSPPE 60
QY      62  HENVKSVDDLHSHLIYNSGPNYDKLTKEKNOEMATLFKDKNVDIYGYEYHLCVLC 121
Db      61  GRGVINSRFLSHDLTFPEYKSYNEVKTELENTALNNYKDKKVDIFGVPYFTCLIPK 120
QY      122  NAE-----RSACIYGGVTNHGHNHLEIPKKIVVKVSDIGQSLSFDIETNKKMVTQAQEL 175
Db      121  SEPDIQNQEGGCMYGGILTFNSEN-ERDKLITVQVITDNRQSLGFTTTNKNMVTIQEL 179
QY      176  DYKRYXLTDNKQLYNGPSKYETGYIKFIPKPKNESFWDFPEPE----FTQSKYLMYIK 232
Db      180  DYKARHLTKRKLKYDFDGSFAFSGYIKFTEKNTSFWDFLFPKKELVPEVPYKFLNIY 239
QY      233  DNETLDSNTSQIEVILYTT 250
Db      240  DNKVDKSKSIKMEVFLNT 257

RESULT 11
A33953
enterotoxin D precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 15-Oct-1999
C:Accession: A33953

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R; Bayles, K.W.; Iandolo, J.J.
J. Bacteriol. 171, 4799-4806, 1989
A; Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin
A; Reference number: A33953; MUID: 89359112; PMID: 2549000
A; Accession: A33953
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-258 <BAY>
C; Cross-references: GB:M28521; NID: g1492109; PIDN: AAB06195.1; PID: g758691
C; Superfamily: enterotoxin_B

Query Match	26.1%	Score 345;	DB 2;	Length 258;
Best Local Similarity	35.6%	Pred. No. 1.1e-18;		
Matches 93:	Conservative	47. M		

QY	8	LKKM-VFFVLVTFLGTLISO-EYFAQQDDP----	PSOLHR-----SSLVKNLQNTYFLYEG	57
DB	1	MKENIILALFFTSVPLNVKANENIDSVKRELHKSELSTALNNKHBY-ADK	58	
QY	58	DPVTHENVKSVDOLLSHLIYN--VSGPNYOKLKTTELKNOEMATLFRKDKNVDIYGEVY	114	
DB	59	NPIIGENK9GDOFLENTLLYKFFPDLLINFEDLLINFNSKEMAQHFKSKNVDYPIRYS	118	
QY	115	HLCYLCSENAERSACIYGVNTHEGNHLPPKIVKVSIDGIO-SLSPD-LETNNKMWTA	172	
DB	119	INCYGGE-IDRTACTYGGVTPHEGNKLERKIPINLWINGVQEVSLDKVOTDKKNVT	177	
QY	173	QELDYKVKRYLTNDKOLYNTGP-SKYETGYIKFTPKNKESFWDFPPEFTOSKYLMI	230	
DB	178	QELDAQRRYLQKDLKLYNNDTLGGKIQRGKIEFSSDGSKVSVDLEVDGDFPEKQLR	237	
QY	231	YKONETLDSNTSQIEVYLTK	251	
DB	238	YSDNKTLSLSTEHLHIDIYLYEK	258	

RESULT 12
C89984
enterotoxin P [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: C89984
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Di, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: C89984
A:Status: preliminary
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-260 <ROR>
A:Cross-references: GB:BA000018; PID:g13701743; PIDN:BA843036.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: sep
C:Superfamily: enterotoxin B

Query Match 25.8%; Score 341; DB 2; Length 260;
Best Local Similarity 34.5%; Pred. No. 2.3e-18;
Matches 92; Conservative 52; Mismatches 85; Indels 38; Gaps 13;

Qy		10	KWFFVLTFTLGLTI-----SQEFAQQDDPPSOLHRSSLVKKNLQNYFLFYEGD	58
Db		5	KTTFILLSFIALTLTITSPFVNCSKEEINGRDLQKKSELOQTAL-SNLRTQYI-HNGS	62
Qy		59	PVTENKSVDOQLSHLIYN--VSGPN-YDKTELKNQEMATLFKDKNVDIYGVEYKH	115
Db		63	AII-ENKESNDQFKNTILFNDEFTGHQWINDLLVDLSKDTANIYKKGVLDYGYVY--	119
Qy		116	LCYLCENAE--RSACIYGGVTIHBEHGNHLETPKKIVVKVSIDGTQSL--SFDIETNKKMVT	171
Db		120	-GYOCTGGTPKTKACMGVTLHDHNNQLEBKVPINLIDGKQNTVPVLGTWNKKVET	178

```

QY      172 AQELDYKVRYLTDNKOLYT-----NGPSKYETGYIKFIPKNKESWFDFPEPEPTQS
DB      ||||| : : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY      179 VQELDQSRYYLHETYNLNTAFNG--KIQRGLIEFHPSGDSVGYDLFG----AQ
DB      ||||| : : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY      228 -----LMIIYKDNETLDNSTQIEVYLTT 250
DB      | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY      233 PDTQLRIYRDNKTIKSNMHHIDIYLT 259
DB      | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |

```

RESULT 13

AB8969
enterotoxin YENT2 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001
C:Accession: AB8969
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaifo, C.; Shiiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus
A:Reference number: AB8958; PMID:21311952; PMID:11418146
A:Accession: AB8969
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <KUR>
A:Cross-references: GB:BA000018; PID:g13701619; PID:BA02912.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: yent2

Query Match	25.5%	Score 337;	DB 2;	Length 136;
Best Local Similarity	49.6%	Pred. No. 2e-18;		
Matches	67;	Conservative 22;	Mismatches 38;	Indels 8; Gaps
QY	125	RSACIYGVTWHEGNHL-----BIPKKIIVKVSIDGIGQSFDIETNKKMVTQAQELD		
Db	2	KRTCMYGVTEHDGNDQDKNNSTDSNINILIKYVENRNSLSFDIPTNKKNITAQEI		
QY	179	VRYKIYTDNKOYITNGPSKIETGYIKFTPKKNESFQWDFPPE--PERTQSKYLMIKYDNN		
Db	62	VRYNLLKHKNLYENSSPYETGYIKFTEGSHGSFYDLMPESGKKFYPTKYLLIYDNN		
QY	237	LDSNTQSEIVYLTTK 251		
Db	122	VEKSKINVEVHLTKK 136		

```

RESULT 14
E89969
  enterotoxin SeO [imported] - Staphylococcus aureus (strain N315)
  C:Species: Staphylococcus aureus
  C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2010
  C:Accession: E89969
  R:Kuroda, M.; Ohka, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.;
  ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.;
  C.: Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
  Lancet 357, 1225-1240, 2001
  A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus au
  A:Reference number: AB8756; MUID:21311952; PMID:11418146
  A:Accession: E89969
  A:Status: preliminary
  A:Molecule type: DNA
  A:Residues: 1-260 <RUR>
  A:Cross-references: GB:BA000018; PID:gl3701623; PIDN:BAB42916.1; GSPDB:GN
  A:Experimental source: strain N315
  C:Genetics:
  A:Gene: seo
  C:Superfamily: enterotoxin B

```

Query Match 25.5%; Score 337; DB 2; Length 260;
Best Local Similarity 36.2%; Pred. NO. 4.5e-18;
Matches 96; Conservative 42; Mismatches 107; Indels 20; Gaps

Query Match	23.9%	Score 316.5;	DB 2;	Length 258;
Best Local Similarity	34.2%;	Presd. No. 1.5e-16;		
Matches	90;	Conservative 49;	Mismatches 101;	Indels 23; Gaps 10;
Qy	1	MENKKVLKKWFF---VLVTFGLGISQEVFAQD-----PDSQLHRSHLVKMLQNIY- 52		
Db	1	MKNIKLMR--LFYIAAIIITLCLINNNVYNAEVDKKDKKSDLDSSKLF-NLTSYVT 57		
Qy	53	-FLYEGDPVTHENVKSDQLLSHLI--YVSGSPNYDKLTKLKNQEMATLFDKKNVDI 108		
Db	58	DTWQLD---ESNKISTDQLLNNITILKINDISVLKTSUKVEFNSDLANQFGKNIDI 114		
Qy	109	YGVEYHLCY-ICENAEERSACIYGGVTNHGHNHEIPKTIWKVSIODIGIOSLSDIFETNK 167		
Db	115	YGLYFNCKVGLTE--EKTSCLYGGVTIHDGNQLDEKVICGVNVFKDGVQGEVITKK 172		
Qy	168	KWYTAQELDYKVRKYLTDNKNQLTNGPISKYETGIYKIPKN--KESWFFDFFPEPEFTQS 225		
Db	173	AKVTQVELDTPKVRKLENYKIYKNTDGTNIQKGCIFPHSHNHQDSFYDLYNVNKGsvGA 232		
Qy	226	KYLMYIKDNETLDSNTSQIEVYL 248.		
Db	233	EFFQFYSDNRVTSSSNYHIDVFL 255		

Search completed: August 21, 2003, 12:50:19
Job time : 37 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 21, 2003, 12:14:04 ; Search time 74 Seconds
(without alignments)
875.287 Million cell updates/sec

Title: US-09-308-830A-13

Perfect score: 1323

Sequence: 1 MNNKKVLKQWFFVLVTF.....KDNLTLSNTSQIEVYLTK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1313	99.2	251	16	O8K6K5
2	1239	93.7	236	2	P97163
3	1238	93.6	236	2	O54779
4	1233	93.2	236	2	O57453
5	1172	88.6	222	2	O9R931
6	1108	83.7	236	2	O54696
7	1053	79.6	222	2	O9S524
8	1053	79.6	222	2	O938P4
9	554	41.9	271	2	O9F0L6
10	552	41.7	266	16	O8NXJ6
11	550	41.6	239	2	O53678
12	549	41.5	239	2	O06532
13	548	41.4	239	2	O06533
14	547	41.3	239	2	O05157
15	547	41.3	239	2	O06531
16	543	41.0	239	2	O06535

17	538	40.7	239	2	O06534	Q06534 staphylococ
18	537	40.6	234	2	O9R5X4	Q9r5x4 staphylococ
19	535.5	40.5	260	2	O54971	Q54971 streptococ
20	530.5	40.1	260	2	O54738	Q54738 streptococ
21	530.5	40.1	260	16	O54739	Q54739 streptococ
22	516.5	39.0	259	2	O936G4	Q936g4 staphylococ
23	470	35.5	258	2	O9ZNF2	Q9znf2 staphylococ
24	470	35.5	258	2	O9EZM3	Q9ezm3 staphylococ
25	468	35.4	233	2	O8RR77	Q8rr77 staphylococ
26	341	25.8	260	16	O9RSU3	Q9rsu3 staphylococ
27	338.5	25.6	261	2	O9EZM8	Q9ezm8 staphylococ
28	337	25.5	136	16	O99T49	Q99t49 staphylococ
29	337	25.5	260	16	O99T46	Q99t46 staphylococ
30	316.5	23.9	258	16	O9EZM4	Q9ezm4 staphylococ
31	315	23.8	250	2	O8GFW6	Q8gfm6 staphylococ
32	312	23.6	260	16	O931M4	Q931m4 staphylococ
33	304.5	23.0	240	16	O9F0L7	Q9f0l7 staphylococ
34	304.5	23.0	268	2	O85217	O85217 staphylococ
35	303.5	22.9	240	16	O8NXJ5	O8nxj5 staphylococ
36	298.5	22.6	241	16	O53585	O53585 staphylococ
37	285.5	21.6	108	2	O9EZM5	Q9ezm5 staphylococ
38	281.5	21.3	217	2	O8RR76	Q8rr76 staphylococ
39	270	20.4	239	16	O99T47	Q99t47 staphylococ
40	269	20.3	239	2	O9EZM7	Q9ezm7 staphylococ
41	259.5	19.6	242	16	O8NVM2	O8nvm2 staphylococ
42	257.5	19.5	242	2	O54476	O54476 staphylococ
43	255.5	19.3	242	2	O93CC5	O93cc5 staphylococ
44	246.5	18.6	256	2	O8VLW7	O8vlw7 staphylococ
45	246	18.6	229	16	O8NWX7	O8nw97 staphylococ

ALIGNMENTS

RESULT 1

ID	O8K6K5	PRELIMINARY;	PRT;	251 AA.
AC	O8K6K5;			
DT	01-OCT-2002 (TReMBLrel. 22, Created)			
DT	01-OCT-2002 (TReMBLrel. 22, Last sequence update)			
DT	01-MAR-2003 (TReMBLrel. 23, Last annotation update)			
DE	Exotoxin type A-phage associated.			
GN	SPEA3 OR SPYM3_1301.			
OS	Streptococcus pyogenes (serotype M3).			
OC	Bacteria: Firmicutes; Lactobacillales; Streptococcaceae;			
OC	Streptococcus			
OX	NCBI_TaxID=198466;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-MGAS315 / Serotype M3;			
RX	MEDLINE=22133808; PubMed=12122206;			
RA	Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,			
RA	Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,			
RA	Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,			
RA	Schlievert P.M., Musser J.M.;			
RT	"Genome sequence of a serotype M3 strain of group A Streptococcus:			
RT	phage-encoded toxins, the high-virulence phenotype, and clone			
RT	emergence."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).			
DR	EMBL; AEO14161; AAM79908.1; -			
DR	InterPro; IPR006177; Bctrl_tox.			
DR	InterPro; IPR006123; Staph/Strep_toxin.			
DR	InterPro; IPR006126; Staph/Strep_tox.			
DR	InterPro; IPR006173; Staph_tox_OB			
DR	Pfam; PF01123; Staph_Strep_toxin; 1.			
DR	Pfam; PF02876; Staph_Strep_tox_C; 1.			
DR	PRINTS; PR00279; BACTRLTOXIN			
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.			
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.			
KW	Complete proteome.			
SQ	SEQUENCE 251 AA; 29260 MW; 05E782CDA01BFCD5 CRC64;			
Query Match	99.2%; Score 1313; DB 16; Length 251;			

Best Local Similarity 99.2%; Pred. No. 1.3e-85;
Matches 249; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNNKKVLLKVVFFVLTGLTISQEVFAQQDDPSQLHRSSLVKLNQNIYFLYEGDPV 60
DB 1 MNNKKVLLKVVFFVLTGLTISQEVFAQQDDPSQLHRSSLVKLNQNIYFLYEGDPV 60
QY 61 THENKVSVDQLSHLLIYVSGPNYDKLTKELKNOEMATLFDKNDVIYGVYHYLCYIC 120
DB 61 THENKVSVDQLSHLLIYVSGPNYDKLTKELKNOEMATLFDKNDVIYGVYHYLCYIC 120
QY 121 ENAERSACIYGVTHNEGNHLEIPKKIVVKSIDIGISLFSFDTNKKMVTAEQELDYKVR 180
DB 121 ENAERSACIYGVTHNEGNHLEIPKKIVVKSIDIGISLFSFDTNKKMVTAEQELDYKVR 180
QY 181 KYLTNKKOLYTNKPSKYETGYIKFIPKNKESFWDFPEFTQSKYLMYKDNETLDSN 240
DB 181 KYLTNKKOLYTNKPSKYETGYIKFIPKNKESFWDFPEFTQSKYLMYKDNETLDSN 240
241 TSQIEVYLTTK 251
DB 241 TSQIEVYLTTK 251

RESULT 2

ID P97163 PRELIMINARY; PRT; 236 AA.
AC P97163;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS156, and MGAS500;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Selaender R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
Streptococcus pyogenes";
RT J. Exp. Med. 174:1271-1274(1991).
RL EMBL; X61556; CAA43754.1; -
DR EMBL; X61557; CAA43755.1; -
DR EMBL; X61560; CAA43758.1; -
DR EMBL; X61555; CAA43753.1; -
DR EMBL; X61558; CAA43756.1; -
DR EMBL; X61559; CAA43757.1; -
DR EMBL; X61554; CAA43752.1; -
DR HSP; P08095; 1B1Z.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Stap/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Stap_strep_toxin; 1.
DR Pfam; PF02876; Stap_strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27454 MW; 3FB3F41ABDC13A84 CRC64;

Query Match 99.7%; Score 1239; DB 2; Length 236;
Best Local Similarity 99.6%; Pred. No. 2.1e-80;
Matches 235; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 KMWFFVLVTFLGLTISQEVFAQQDDPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSV 68
DB 1 KMWFFVLVTFLGLTISQEVFAQQDDPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSV 60
QY 69 DOLLSHLLIYVSGPNYDKLTKELKNOEMATLFDKNDVIYGVYHYLCYICENAESAC 128
DB 61 DOLLSHLLIYVSGPNYDKLTKELKNOEMATLFDKNDVIYGVYHYLCYICENAESAC 120
QY 129 IYGGVTNHEGNHLEIPKKIVVKSIDIGISLFSFDTNKKMVTAEQELDYKVRKYLTDNKK 188
DB 121 IYGGVTNHEGNHLEIPKKIVVKSIDIGISLFSFDTNKKMVTAEQELDYKVRKYLTDNKK 180
QY 189 LYTNKPSKYETGYIKFIPKNKESFWDFPEFTQSKYLMYKDNETLDSNTSQI 244
DB 181 LYTNKPSKYETGYIKFIPKNKESFWDFPEFTQSKYLMYKDNETLDSNTSQI 236

RESULT 3

Q54779 PRELIMINARY; PRT; 236 AA.
AC Q54779; Q54613; Q54736; Q54740; Q54741;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS624 AND MGAS158 AND MGAS485 AND MGAS491, and MGAS495;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Selaender R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
Streptococcus pyogenes";
RT J. Exp. Med. 174:1271-1274(1991).
RL EMBL; X61569; CAA43767.1; -
DR EMBL; X61572; CAA43770.1; -
DR EMBL; X61568; CAA43766.1; -
DR EMBL; X61570; CAA43768.1; -
DR EMBL; X61571; CAA43769.1; -
DR HSP; P08095; 1B1Z.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Stap/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Stap_strep_toxin; 1.
DR Pfam; PF02876; Stap_strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27468 MW; 29DF2AD575623A84 CRC64;

Query Match 93.6%; Score 1238; DB 2; Length 236;
Best Local Similarity 99.2%; Pred. No. 2.5e-80;
Matches 234; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 KMWFFVLVTFLGLTISQEVFAQQDDPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSV 68
DB 1 KMWFFVLVTFLGLTISQEVFAQQDDPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSV 60
QY 69 DOLLSHLLIYVSGPNYDKLTKELKNOEMATLFDKNDVIYGVYHYLCYICENAESAC 128
DB 61 DOLLSHLLIYVSGPNYDKLTKELKNOEMATLFDKNDVIYGVYHYLCYICENAESAC 120

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Qy 129 IYGVVTHNHNLEIPKIVVKSIDIGISLSDIETNKKMVAQELDYKVRKYLTDNKQ 188
Db 121 IYGVVTHNHNLEIPKIVVKSIDIGISLSDIETNKKMVAQELDYKVRKYLTDNKQ 180
Qy 189 LYTNPSKYETGYIKFIPKNKESFWDFPEFTQSKYLMYKDNETLDSNTSQI 244
Db 181 LYTNPSKYETGYIKFIPKNKESFWDFPEFTQSKYLMYKDNETLDSNTSQI 236

RESULT 4
Q57453
ID Q57453 PRELIMINARY; PRT; 236 AA.
AC Q57453;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS496;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
RL J. Exp. Med. 174:1271-1274 (1991).
DR EMBL; X61562; CAA43760.1; -
DR EMBL; X61563; CAA43761.1; -
DR EMBL; X61567; CAA43765.1; -
DR EMBL; X61561; CAA43759.1; -
DR EMBL; X61564; CAA43762.1; -
DR EMBL; X61565; CAA43763.1; -
DR EMBL; X61566; CAA43764.1; -
DR HSP; P08095; IBI2.
DR InterPro; IPR006177; Bcrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_toxin; 1.
DR Pfam; PF02876; Staph_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1 1
FT CHAIN 23 236
FT SIGNAL <1 22 POTENTIAL.
FT TYPE A EXOTOXIN.
FT NON_TER 236 236
FT SEQUENCE 236 AA; 27484 MW; 2EF7P41AAC853600 CRC64;

Query Match 93.2%; Score 1233; DB 2; Length 236;
Best Local Similarity 99.2%; Pred. No. 5.6e-80;
Matches 234; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 KKMVFVLTFLGLTISQEVFAQQDDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 68
Db 1 KKMVFVLTFLGLTISQEVFAQQDDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 60
Qy 69 DQLLSHLIYNVSGPNVDKLTCLKNQEMATLFKDKNVDIYGYEYHLCYLCENASAC 128
Db 61 DQLLSHLIYNVSGPNVDKLTCLKNQEMATLFKDKNVDIYGYEYHLCYLCENASAC 120
Qy 129 IYGVVTHNHNLEIPKIVVKSIDIGISLSDIETNKKMVAQELDYKVRKYLTDNKQ 188
Db 121 IYGVVTHNHNLEIPKIVVKSIDIGISLSDIETNKKMVAQELDYKVRKYLTDNKQ 180
Qy 189 LYTNPSKYETGYIKFIPKNKESFWDFPEFTQSKYLMYKDNETLDSNTSQI 244

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Db 181 LYTNPSKYETGYIKFIPKNKESFWDFPEFTQSKYLMYKDNETLDSNTSQI 236
|||||
RESULT 5
Q9R931
ID Q9R931 PRELIMINARY; PRT; 222 AA.
AC Q9R931;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Exotoxin A (Fragment).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D709;
RX MEDLINE=99137798; PubMed=9952369;
RA Bessen D.E., Izzo M.W., Fiorentino T.R., Carling R.M.,
RA Hollingshead S.K., Beall B.;
RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue
RT tropism in group A streptococci.";
RL J. Infect. Dis. 179:627-636 (1999).
DR EMBL; AF055698; AAD11624.1; -
DR HSP; P08095; IBI2.
DR InterPro; IPR006177; Bcrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_toxin; 1.
DR Pfam; PF02876; Staph_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1 1
FT NON_TER 222 222
FT SEQUENCE 222 AA; 25759 MW; 48BB7ADDCD91FBA3 CRC64;

Query Match 88.6%; Score 1172; DB 2; Length 222;
Best Local Similarity 99.5%; Pred. No. 1.1e-75;
Matches 221; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 GLTISQEVFAQQDDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHLIYNV 80
Db 1 GLTISQEVFAQQDDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHLIYNV 60
Qy 81 SGPNDKLTCLKNQEMATLFKDKNVDIYGYEYHLCYLCENASACIYGVVTHNHN 140
Db 61 SGPNDKLTCLKNQEMATLFKDKNVDIYGYEYHLCYLCENASACIYGVVTHNHN 120
Qy 141 LEIPKIVVKSIDIGISLSDIETNKKMVAQELDYKVRKYLTDNKQLYTNPSKYETG 200
Db 121 LEIPKIVVKSIDIGISLSDIETNKKMVAQELDYKVRKYLTDNKQLYTNPSKYETG 180
Qy 201 YIKFIPKNKESFWDFPEFTQSKYLMYKDNETLDSNTS 242
Db 181 YIKFIPKNKESFWDFPEFTQSKYLMYKDNETLDSNTS 222
|||||
RESULT 6
Q54696
ID Q54696 PRELIMINARY; PRT; 236 AA.
AC Q54696;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

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OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS156;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Selandier R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
RL J. Exp. Med. 174:1271-1274(1991).
DR EMBL; X61573; CAA3771.1; -.
DR HSP; P08095; IB12.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Stap/Strep_toxin.
DR InterPro; IPR006126; Staph/Strept_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Stap_Strp_toxin; 1.
DR Pfam; PF02876; Stap_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27575 MW; 70F54120E79127DF CRC64;

Query Match 83.7%; Score 1108; DB 2; Length 236;
Best Local Similarity 88.6%; Pred. No. 4.1e-71;
Matches 209; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 9 KKMVEFLVTFGLTISQEVFAQQDPNPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSV 68
DB 1 KKIVYFLAIFLGLTTSQEVFAQQDPNPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSV 60

QY 69 DQLLSHLIYNVSGPNYDKLTKLKNQEMATLFDKKNVDIYGVYHYHLCYLGENAERSAC 128
DB 61 DQLLSHDLIYNVSGLVNDKLTCLKNREMTLFFKNKNVDIYGVYHYHLCYLCRNARRAC 120

QY 129 IYGVNTHNHNLEIPKKIYKVSIDGQSLSFDIETNKKMTAQELDYKVRKLYTDNKKQ 188
DB 121 IYGVNTHNHNLEIPKNILYKVSIDGQSLSFDIETSKKMTAQELDYKVRKHLTDNKK 180

189 LYNGSPSKYETGYIKFIPKNKSEFWDFPEPEFTQSKYLMYKDNETLDSNTSQI 244
181 LYNGSPSKYETGYIKFISKDKETFWDFPEPEFNQVKYLMYKDNETLDSNTSQI 236

RESULT 7
Q9S5Z4 PRELIMINARY; PRT; 222 AA.
AC Q9S5Z4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Exotoxin type A (Fragment).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D633;
RX MEDLINE=99137798; PubMed=9952369;
RA Bessen D.E., Izzo M.W., Fiorentino T.R., Caringal R.M.,
RA Hollingshead S.K., Beall B.;
RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue
RT tropism in group A streptococci.";
RL J. Infect. Dis. 179:627-636(1999).
DR EMBL; AF029051; AAD21315.1; -.

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DR HSP; P08095; IB12.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Stap/Strep_toxin.
DR InterPro; IPR006126; Staph/Strept_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Stap_Strp_toxin; 1.
DR Pfam; PF02876; Stap_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1 1
FT NON_TER 222 222
SQ SEQUENCE 222 AA; 25884 MW; 121F8460992818F8 CRC64;

Query Match 79.6%; Score 1053; DB 2; Length 222;
Best Local Similarity 89.2%; Pred. No. 3e-67;
Matches 198; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 21 GLTISQEVFAQQDPNPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSV DQLLSHLIYNV
DB 1 GLTTSQEVFAQQDPNPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSV DQLLSHDLIYNV

QY 81 SGPNTDKLTKLKNQEMATLFDKKNVDIYGVYHYHLCYLGENAERSACIYGVNTHNHN
DB 61 SGLNYDKLTKLKNREMTLFFKNKNVDIYGVYHYHLCYLCRNARRACIYGVNTHNHN

QY 141 LEIPKKIYKVSIDGQSLSFDIETNKKMTAQELDYKVRKLYTDNKKQLYTNGSPSKYETG
DB 121 LEIPKNILYKVSIDGQSLSFDIETSKKMTAQELDYKVRKHLTDNKKQLYTNGSPSKYETG

QY 201 YIKFIPKNKSEFWDFPEPEFTQSKYLMYKDNETLDSNTS 242
DB 181 YIKFISKDKETFWDFPEPEFNQVKYLMYKDNETLDSNTS 222

RESULT 8
Q938P4 PRELIMINARY; PRT; 222 AA.
AC Q938P4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Pyrogenic exotoxin A (Fragment).
GN SPEA.
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=119602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4951;
RA Kalia A., Bessen D.E.;
RT "Presence of streptococcal pyrogenic exotoxin A and C genes in human
RT isolates of group G streptococci.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY049745; AAL06068.1; -.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Stap/Strep_toxin.
DR InterPro; IPR006126; Staph/Strept_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Stap_Strp_toxin; 1.
DR Pfam; PF02876; Stap_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1 1
FT NON_TER 222 222
SQ SEQUENCE 222 AA; 25884 MW; 121F8460992818F8 CRC64;

Query Match 79.6%; Score 1053; DB 2; Length 222;
Best Local Similarity 89.2%; Pred. No. 3e-67;
Matches 198; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

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Qy 21 GLTISQEVFAQQDPDPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSVQDQLLSHLIYNV 80
Db 1 GLTISQEVFAQQDPDPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSVQDQLLSHLIYNV 60
Qy 81 SGPNDYKLTQKQEMATLFDKNDVIYGVYHYHLCYLCENASACIYGGVTHHGNH 140
Db 61 SGLNDYKLTQKQEMATLFDKNDVIYGVYHYHLCYLCENASACIYGGVTHHGNH 120
Qy 141 LEIPKIVKVSIDIGISQSLDIETNKKWTAQELDYKVKRYLTDNQLYNGSPKYETG 200
Db 121 LEIPKIVKVSIDIGISQSLDIETNKKWTAQELDYKVKRYLTDNQLYNGSPKYETG 180
Qy 201 YIKFIPKNKESFDFEPEPEFTOSKYLMIYKDNELDSNTS 242
Db 181 YIKFIPKNKESFDFEPEPEFTOSKYLMIYKDNELDSNTS 222
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RESULT 9

```
Q9F0L6 PRELIMINARY; PRT; 271 AA.
AC Q9F0L6;
DT 01-MAR-2001 (TremBrel. 16, Created)
DT 01-MAR-2001 (TremBrel. 16, Last sequence update)
DT 01-MAR-2003 (TremBrel. 23, Last annotation update)
DE Staphylococcus aureus C-ovine.
GN SEC-BOV.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2056668; PubMed=1114901;
RA Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
RA Meaney W.J., Smyth C.J.;
RT "Characterization of a putative pathogenicity island from bovine
RT Staphylococcus aureus encoding multiple superantigens."
RL J. Bacteriol. 183:63-70(2001).
DR HSSP; AF217235; AAG29599.1; -.
DR HSSP; P34071; 1SE2.
DR InterPro; IPR006177; Bcrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_toxin; 1.
DR Pfam; PF02876; Staph_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 271 AA; 31267 MW; 3493F622B8B042F10 CRC64;
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Query Match 41.9%; Score 554; DB 2; Length 271;
Best Local Similarity 44.9%; Pred. No. 9,3e-32;
Matches 115; Conservative 51; Mismatches 72; Indels 18; Gaps 8;
Qy 11 MVF-FVLVTFGLTISQEVFAQQDPDPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSV 68
Db 17 LIFALILVLPFPNVLAEE---SOPDTPDELHKASKFTGLMENMKVLYDDRVSVATKVKSV 73
Qy 69 DQLLSHLIYNVSG---PNYDKLTKELKNQEMATLFDKNDVIYGVYHYHLCYLC--ENA 123
Db 74 DKFLAHLIYNISDKLKNYDKVKTELLNEDLAKYKDEVDVYVYNSYVNCYFSSKDNV 133
Qy 124 ER----SACIYGGVTHHGNHLEIPK--KIVVKVSIQSLSFSDIETNKKWTAQELDY 177
Db 134 GKVTGGKTCMYGGITKHEGHNFDGKNGLNQNIYVYENKRNITISFEVQDKKSVTAQELDI 193
Qy 178 KVRKYLTDNQLYNGSPKYETGYIKFIPKNKESFDFEPEPE--EFTQSKYLMIYKDNK 235
Db 194 KARNFLKNKLYEFNSSPYETGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMYNDNK 253
Qy 236 TLDNNTSQIEVYLTK 251
Db 254 TVDSKSKVIEVHLTK 269
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RESULT 10

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Q8NXJ6 PRELIMINARY; PRT; 266 AA.
AC Q8NXJ6;
DT 01-OCT-2002 (TremBrel. 22, Created)
DT 01-OCT-2002 (TremBrel. 22, Last sequence update)
DT 01-MAR-2003 (TremBrel. 23, Last annotation update)
DE ENTEROTOXIN TYPE C PRECURSOR.
GN SEC4 OR MW0759.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
DR EMBL; AP004824; BAB94624.1; -.
DR InterPro; IPR006177; Bcrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_toxin; 1.
DR Pfam; PF02876; Staph_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 266 AA; 30670 MW; 4C654659AA48120F CRC64;
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Query Match 41.7%; Score 552; DB 16; Length 266;
Best Local Similarity 44.5%; Pred. No. 1.3e-31;
Matches 114; Conservative 51; Mismatches 73; Indels 18; Gaps 8;
Qy 11 MVF-FVLVTFGLTISQEVFAQQDPDPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSV 68
Db 12 LIFALILVLPFPNVLAEE---SOPDTPDELHKASKFTGMNMYLYDDRVSVATKVKSV 68
Qy 69 DQLLSHLIYNVSG---PNYDKLTKELKNQEMATLFDKNDVIYGVYHYHLCYLC--ENA 123
Db 69 DKFLAHLIYNISDKLKNYDKVKTELLNEDLAKYKDEVDVYVYNSYVNCYFSSKDNV 128
Qy 124 ER----SACIYGGVTHHGNHLEIPK--KIVVKVSIQSLSFSDIETNKKWTAQELDY 177
Db 129 GKVTGGKTCMYGGITKHEGHNFDGKNGLNQNIYVYENKRNITISFEVQDKKSVTAQELDI 188
Qy 178 KVRKYLTDNQLYNGSPKYETGYIKFIPKNKESFDFEPEPE--EFTQSKYLMIYKDNK 235
Db 189 KARNFLKNKLYEFNSSPYETGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMYNDNK 248
Qy 236 TLDNNTSQIEVYLTK 251
Db 249 TVDSKSKVIEVHLTK 264
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RESULT 11

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Q53678 PRELIMINARY; PRT; 239 AA.
AC Q53678;
DT 01-NOV-1996 (TremBrel. 01, Created)
DT 01-NOV-1996 (TremBrel. 01, Last sequence update)
DT 01-MAR-2003 (TremBrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
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RP SEQUENCE FROM N.A.
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RL biological and evolutionary implications.";
DR Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13376; AAA26620.1; -.
DR HSSP; P34071; ISE2.
DR InterPro; IPR006177; Bcstrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR NON_TER 1
SQ SEQUENCE 239 AA; 27618 MW; A13E7EB25C6989C2 CRC64;

Query Match 41.6%; Score 550; DB 2; Length 239;
Best Local Similarity 47.0%; Pred. No. 1.5e-31;
Matches 111; Conservative 45; Mismatches 66; Indels 14; Gaps 6;

QY 30 AQDDPDSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVQDQLSHHLYNVSG---PNY 85
DB 2 SQDPTPDELHKASKFTGLMNNKVLDDRYVSATKVKSVDFLAHDLIYNISDKLKNY 61
QY 86 DKLTTELKNOEMATLFKDKNDVIYGVYHLCYLC--ENAEER----SACIYGGVTNHG 139
DB 62 DKVTELLNEDLAKKYDEVVDVYGSNYVYCNFYSSKDNVGVTKGCTCMYGGITKHG 121
QY 140 HLEIPK--KIVVKVSDIGQISLFDIETNKKMVTQAQELDYKVRKYLTDNKLTYNGPSKY 197
DB 122 HFDNGNLQNLVLRVYENKRNITISFEVQTDKSVTAQELDIKARNFLINKNLYEFNSP 181
QY 198 ETGYIKFIPKNKESFWDFFPEP--EFTQSKYLMYKDNETLDSNTSQIEVYLTK 251
DB 182 ETGYIKFTENNGTWFYDMMPAGDKFQDSKYLMMYNDNKTVDKSVKIEVHLTK 237

RESULT 12
Q06532 PRELIMINARY; PRT; 239 AA.
AC Q06532;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=740N;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RL biological and evolutionary implications.";
DR Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13375; AAA26619.1; -.
DR HSSP; P34071; ISE2.
DR InterPro; IPR006177; Bcstrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR NON_TER 1
SQ SEQUENCE 239 AA; 27642 MW; C77009F46BC8D645 CRC64;

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Query Match 41.5%; Score 549; DB 2; Length 239;
Best Local Similarity 47.0%; Pred. No. 1.8e-31;
Matches 111; Conservative 44; Mismatches 67; Indels 14; Gaps

QY 30 AQDDPDSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVQDQLSHHLYNVSG---PNY
DB 2 SQDPTPDELHKASKSEFTGTMDNMKLYLDDHYVSATKVKSVDFLAHDLIYNISDKLKN
QY 86 DKLTTELKNOEMATLFKDKNDVIYGVYHLCYLC--ENAEER----SACIYGGVTNHG
DB 62 DKVTELLNEDLAKKYDEVVDVYGSNYVYCNFYSSKDNVGVTKGCTCMYGGITKHG
QY 140 HLEIP--KKIVVKVSDIGQISLFDIETNKKMVTQAQELDYKVRKYLTDNKLTYNGPSK
DB 122 HFDNGNLQNLVLRVYENKRNITISFEVQTDKSVTAQELDIKARNFLINKNLYEFNSP
QY 198 ETGYIKFIPKNKESFWDFFPEP--EFTQSKYLMYKDNETLDSNTSQIEVYLTK 251
DB 182 ETGYIKFTENNGTWFYDMMPAGDKFQDSKYLMMYNDNKTVDKSVKIEVHLTK 237

RESULT 13
Q06533 PRELIMINARY; PRT; 239 AA.
AC Q06533;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MN0Copoland;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RL biological and evolutionary implications.";
DR Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13378; AAA26622.1; -.
DR HSSP; P34071; ISTE.
DR InterPro; IPR006177; Bcstrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR NON_TER 1
SQ SEQUENCE 239 AA; 27651 MW; A21A954386A8E625 CRC64;

Query Match 41.4%; Score 548; DB 2; Length 239;
Best Local Similarity 46.6%; Pred. No. 2.1e-31;
Matches 110; Conservative 45; Mismatches 67; Indels 14; Gaps

QY 30 AQDDPDSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVQDQLSHHLYNVSG---PNY
DB 2 SQDPTPDELHKASKSEFTGTMDNMKLYLDDHYVSATKVKSVDFLAHDLIYNISDKLKN
QY 86 DKLTTELKNOEMATLFKDKNDVIYGVYHLCYLC--ENAEER----SACIYGGVTNHG
DB 62 DKVTELLNEDLAKKYDEVVDVYGSNYVYCNFYSSKDNVGVTKGCTCMYGGITKHG
QY 140 HLEIP--KKIVVKVSDIGQISLFDIETNKKMVTQAQELDYKVRKYLTDNKLTYNGPSK
DB 122 HFDNGNLQNLVLRVYENKRNITISFEVQTDKSVTAQELDIKARNFLINKNLYEFNSP
QY 198 ETGYIKFIPKNKESFWDFFPEP--EFTQSKYLMYKDNETLDSNTSQIEVYLTK 251
DB 182 ETGYIKFTENNGTWFYDMMPAGDKFQDSKYLMMYNDNKTVDKSVKIEVHLTK 237

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Db 182 ETGYIKFIENNGNTFWYDMPAPGDKFDQSKYLMYNDNKTVDKRVKIEVHLTK 237
RESULT 14
O05157 PRELIMINARY; PRT; 239 AA.
AC O05157;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Type C enterotoxin (Fragment).
OS Staphylococcus intermedius.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1285;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95-011195;
RA Edwards V.M., Deringer J.R., Callantine S.D., Deobald C.F.,
RA Berger P.H., Kapur V., Stauffer C.V., Bohach G.A.;
RT "Characterization of the type C enterotoxin (SEC-canine) produced by
RT Staphylococcus intermedius pyoderma isolates."
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RR EMBL; U91526; AAB50248.1;
RR HSP; P23313; IJCK
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
FT 1
SQ SEQUENCE 239 AA; 27536 MW; D660644660DE4191 CRC64;

Query Match 41.3%; Score 547; DB 2; Length 239;
Best Local Similarity 47.5%; Pred. No. 2.5e-31;
Matches 112; Conservative 42; Mismatches 68; Indels 14; Gaps 6;

QY 30 AQDDPPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVDDLSSHLLIYNVSG---PNY 85
DB 2 SQDDPMPDDLKSEFTGTGNMKCLYDDHYVSVATKVKSVDKFLAHLIYINISDKRLK 61

QY 86 DLKLTENKQEMATLFRKDNVDIYGYEYHLCYLC--ENAE-----SACIYGGVTNHEGN 139
DB 62 DKVKTLLNEDLAKKYKDEVVDYVGSNYVNCYFSSKDNVGVKGTCTMYGTTKHEGN 121

QY 140 HLEIP--KKIVKVSIDGSLSDIETNKKMTAQELDYKVKYLTDNKQLYTNGPSKY 197
DB 122 HFDGNLQNLVIRVYENKRNITISFVQTDKKSQVTAQELDIKARNFLINKNLYEFN 181

QY 198 ETGYIKFIENNGNTFWYDMPAPGDKFDQSKYLMYNDNKTVDKRVKIEVHLTK 251
DB 182 ETGYIKFIENNGNTFWYDMPAPGDKFDQSKYLMYNDNKTVDKRVKIEVHLTK 237

RESULT 15
O06531 PRELIMINARY; PRT; 239 AA.
AC O06531;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4446;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
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RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13374; AAA26618.1;
DR HSP; P34071; ISE2.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
FT 1
SQ SEQUENCE 239 AA; 27612 MW; BB7BD6204731ED24 CRC64;

Query Match 41.3%; Score 547; DB 2; Length 239;
Best Local Similarity 47.0%; Pred. No. 2.5e-31;
Matches 111; Conservative 44; Mismatches 67; Indels 14; Gaps 6;

QY 30 AQDDPPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVDDLSSHLLIYNVSG---PNY 85
DB 2 SQDDPMPDDLKSEFTGTGNMKCLYDDHYVSVATKVKSVDKFLAHLIYINISDKRLK 61

QY 86 DLKLTENKQEMATLFRKDNVDIYGYEYHLCYLC--ENAE-----SACIYGGVTNHEGN 139
DB 62 DKVKTLLNEDLAKKYKDEVVDYVGSNYVNCYFSSKDNVGVKGTCTMYGTTKHEGN 121

QY 140 HLEIP--KKIVKVSIDGSLSDIETNKKMTAQELDYKVKYLTDNKQLYTNGPSKY 197
DB 122 HFDGNLQNLVIRVYENKRNITISFVQTDKKSQVTAQELDIKARNFLINKNLYEFN 181

QY 198 ETGYIKFIENNGNTFWYDMPAPGDKFDQSKYLMYNDNKTVDKRVKIEVHLTK 251
DB 182 ETGYIKFIENNGNTFWYDMPAPGDKFDQSKYLMYNDNKTVDKRVKIEVHLTK 237

Search completed: August 21, 2003, 12:49:34
Job time : 76 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 21, 2003, 10:23:04 ; Search time 30 seconds
(without alignments)
393.457 Million cell updates/sec

Title: US-09-308-830A-13

Perfect score: 1323

Sequence: 1 MENKKVLKMKVFFVLVTF.....KDNFTLSDNTSQIEVYLTK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1314	99.3	251	1 SPEA_STRPY	P08095 streptococ
2	575.5	43.5	266	1 ETXB_STAAU	P01552 staphylococ
3	550.5	41.6	266	1 ETC3_STAAM	P23313 staphylococ
4	548	41.4	266	1 ETC2_STAAU	P34071 staphylococ
5	547	41.3	266	1 ETC1_STAAU	P01553 staphylococ
6	480	36.3	258	1 ETXG_STAAM	O85382 staphylococ
7	345	26.1	258	1 ETDY_STAAU	P20723 staphylococ
8	313	23.7	257	1 ETXE_STAAU	P12993 staphylococ
9	312	23.6	257	1 ETXA_STAAU	P13163 staphylococ
10	214	16.2	235	1 SPEB_STRPY	P13380 streptococ
11	213.5	16.1	236	1 SPEH_STRPY	O9x5c8 streptococ
12	162	12.2	234	1 SPEG_STRPY	O9x5c7 streptococ
13	116	8.8	234	1 TSST_STAAU	P06886 staphylococ
14	102.5	7.7	1790	1 USO1_YEAST	P25386 saccharomyc
15	101	7.6	894	1 DSC1_HUMAN	O08554 homo sapien
16	100.5	7.6	396	1 PRC_ECOLI	P17223 escherichia
17	96	7.3	427	1 V53A_HSV7J	P52517 human herpe
18	96	7.3	908	1 DP01_BORBU	O51498 borrelia bu
19	95.5	7.2	434	1 PURA_WIGBR	O8d322 wigglewort
20	95.5	7.2	999	1 HGP2_HAEIN	P44809 haemophilus
21	95	7.2	554	1 Y478_RICPR	O9z466 rickettsia
22	94.5	7.1	2151	1 RRPL_SEOUB	P27314 seoul virus
23	93	7.0	500	1 TACY_CLOPE	P19995 clostridium
24	92.5	7.0	968	1 RNE_BUCAP	O8k9j9 buchnera ap
25	92	7.0	660	1 PRIA_BORBU	O45032 borrelia bu
26	91.5	6.9	405	1 DBR1_YEAST	P24309 saccharomyc
27	91	6.9	384	1 SCS7_YEAST	O03529 saccharomyc
28	91	6.9	1956	1 ATX1_PLAFA	O04956 plasmodium
29	91	6.9	3255	1 POLG_LMOV	P31999 l genome po
30	90.5	6.8	807	1 HYSA_STAAU	O59801 staphylococ
31	90.5	6.8	3255	1 POLG_LMVE	P89876 l genome po
32	90	6.8	286	1 Y907_METJA	O58317 methanococ
33	90	6.8	376	1 CARA_WIGBR	O8d3h7 wigglewort

ALIGNMENTS

RESULT 1

ID	SPEA_STRPY	STANDARD;	PRT;	251 AA.
AC	P08095;			
DT	01-AUG-1988 (Rel. 08, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin)			
DE	(SPE A).			
GN	SPEA OR SPYM18_0393.			
OS	Streptococcus pyogenes, and			
OS	Streptococcus pyogenes (serotype M18).			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OC	Streptococcus.			
OX	NCBI_TaxID=1314, 186103;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86166804; PubMed=3514452;			
RA	Weeks C.R., Ferretti J.J.;			
RA	"Nucleotide sequence of the type A streptococcal exotoxin			
RT	(erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage			
RT	T12.";			
RL	Infect. Immun. 52:144-150(1986).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86284313; PubMed=3526093;			
RA	Johnson L.P., L'Italien J.J., Schlievert P.M.;			
RT	"Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is			
RT	related to Staphylococcus aureus enterotoxin B.";			
RL	Mol. Gen. Genet. 203:354-356(1986).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MGAS8232 / Serotype M18;			
RX	MEDLINE=21927593; PubMed=11917108;			
RA	Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,			
RA	Syva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,			
RA	Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,			
RA	Kapur V., Daly J.A., Veasy L.G., Musser J.M.;			
RT	"Genome sequence and comparative microarray analysis of serotype M18			
RT	group A Streptococcus strains associated with acute rheumatic fever			
RT	outbreaks.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).			
RN	[4]			
RP	X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).			
RX	MEDLINE=99094887; PubMed=9878045;			
RA	Papageorgiou A.C., Collins C.M., Gutman D.M., Kline J.B.,			
RA	O'Brien S.M., Tranter H.S., Acharya K.R.;			
RT	"Structural basis for the recognition of superantigen streptococcal			
RT	pyrogenic exotoxin A (SpeA) by MHC class II molecules and T-cell			
RT	receptors.";			
RL	EMBO J. 18:9-21(1999).			
CC	- - SUBUNIT: Binds to major histocompatibility complex class II beta			
CC	chain.			
CC	- - DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE			
CC	THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET			
CC	FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE			

34	90	6.8	440	1	STRP_STRPY	P10520 streptococ
35	89.5	6.8	439	1	NADB_CLOPE	O8xne2 clostridium
36	89.5	6.8	642	1	SYT_BUCAP	P46244 buchnera ap
37	89	6.7	307	1	OPPE_STRP8	O8p215 streptococ
38	88.5	6.7	487	1	DNLI_BPT6	P19088 bacterioph
39	88.5	6.7	495	1	Y243_AQUAE	O66606 aquifex aeo
40	88.5	6.7	540	1	MTAL_ACICA	P25201 acinetobact
41	88.5	6.7	993	1	HGBC_HAEIN	O9k1v0 haemophilus
42	88	6.7	181	1	RM06_ACACA	P46765 acanthamoeb
43	88	6.7	322	1	GP18_CAEEL	P49048 caenorhabdi
44	88	6.7	377	1	Y835_METJA	O58245 methanococ
45	87.5	6.6	357	1	SP11_RABPU	P42928 rabbitpox v

DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC FEVER.

-1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.

-1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN FAMILY.

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EMBL; UA0453; AAC4868.1; -
 EMBL; X03929; CAA27568.1; -
 EMBL; AE009982; AAL97141.1; -
 PDB; 1B12; 24-NOV-99.
 PDB; 1FNU; 17-NOV-00.
 PDB; 1FNV; 17-NOV-00.
 PDB; 1FNW; 17-NOV-00.
 PDB; 1HAS; 03-APR-02.
 PDB; 1LOX; 03-APR-02.
 InterPro; IPR006177; Bctrl_tox.
 InterPro; IPR006123; Staph/Strep_toxin.
 InterPro; IPR006136; Staph/Strep_tox.
 InterPro; IPR006173; Staph_tox_OB.
 Pfam; PF02876; Staph_strep_tox_C; 1.
 Pfam; PF01123; Staph_strep_toxin; 1.
 PRINTS; PR00279; BACTRLTOXIN.
 PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 Toxin; Signal; 3D-structure; Complete proteome.

SIGNAL 1 30
 CHAIN 31 251
 DISULFID 117 128
 CONFLICT 6 6
 CONFLICT 17 18
 CONFLICT 25 35
 CONFLICT 40 40
 CONFLICT 43 43
 CONFLICT 47 59

CONFLICT 129 129
 CONFLICT 165 178

HELIX 36 38
 HELIX 42 44
 TURN 48 48
 HELIX 49 56
 STRAND 60 66
 STRAND 69 69
 TURN 73 74
 STRAND 75 78
 STRAND 82 82
 TURN 83 84
 STRAND 85 85
 STRAND 87 91
 HELIX 95 101
 TURN 102 103
 STRAND 105 110
 STRAND 113 113
 TURN 115 116
 STRAND 126 130
 STRAND 133 135
 TURN 137 138
 STRAND 140 153
 TURN 154 155
 STRAND 156 167
 STRAND 169 171
 STRAND 172 187
 HELIX 199 205
 STRAND 212 215

EXOTOXIN TYPE A.
 K -> E (IN REF. 2).
 VT -> MK (IN REF. 2).
 SOEVFAQQDPD -> LPKGCSTRPK (IN REF. 2).
 H -> Q (IN REF. 2).
 S -> N (IN REF. 2).
 NLQNTFLYEGDP -> TFKIYIFEMRVTL (IN REF. 2).
 I -> L (IN REF. 2).
 TNKKMVTQAELDYK -> QIKNGNCSRIYST (IN REF. 2).

FT HELIX 224 227
 FT HELIX 228 231
 FT TURN 232 233
 FT STRAND 236 238
 FT TURN 239 241
 FT STRAND 243 249
 SQ SEQUENCE 251 AA; 29246 MW; 54001FE4CCCBFC03 CRC64;

Query Match 99.3%; Score 1314; DB 1; Length 251;
 Best Local Similarity 99.6%; Pred. No. 1.2e-92;
 Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNNKKVLKMWPFVLVTLGLTISQEVFAQQDPDPSQLHRSLSLVNQLNIYFLYEC
 DB 1 MNNKKVLKMWPFVLVTLGLTISQEVFAQQDPDPSQLHRSLSLVNQLNIYFLYEC
 QY 61 THENVKVDQLSHHLIYVSGPNYDKLKTTELKNQEMATLFDKKNVDIYGVYHHLC
 DB 61 THENVKVDQLSHHLIYVSGPNYDKLKTTELKNQEMATLFDKKNVDIYGVYHHLC
 QY 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVVKVSDIGIQSLSFDTETNKKMVTQAELDY
 DB 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVVKVSDIGIQSLSFDTETNKKMVTQAELDY
 QY 181 KYLTDNKQLYNGSPSKYETGYIKFIPKNKESWFDFPEPEFTQSKYLIYKDNETI
 DB 181 KYLTDNKQLYNGSPSKYETGYIKFIPKNKESWFDFPEPEFTQSKYLIYKDNETI
 QY 241 TSQIEVYLTK 251
 DB 241 TSQIEVYLTK 251

RESULT 2
 ETXB STAAU STANDARD; PRT; 266 AA.
 ID AC P01552;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Enterotoxin type B precursor (SEB).
 GN ENTB.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86168029; PubMed=3957869;
 RA Jones C.L., Khan S.A.;
 RT "Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.";
 RL J. Bacteriol. 166:29-33(1986).
 RN [2]
 RP SEQUENCE OF 40-91 FROM N.A.
 RX MEDLINE=85298255; PubMed=3898073;
 RA Raneilli D.M., Jones C.L., Johns M.B., Mussey G.J., Khan S.A.;
 RT "Molecular cloning of staphylococcal enterotoxin B gene in Escherichia coli and staphylococcus aureus.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854(1985).
 RN [3]
 RP SEQUENCE OF 28-266 (S-6).
 RX MEDLINE=71007902; PubMed=5470821;
 RA Huang I.-Y., Bergdoll M.S.;
 RT "The primary structure of staphylococcal enterotoxin B. 3. The cyanogen bromide peptides of reduced and aminoethylated enterotoxin B, and the complete amino acid sequence.";
 RL J. Biol. Chem. 245:3518-3525(1970).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=93063291; PubMed=1436058;
 RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
 RT "Crystal structure of staphylococcal enterotoxin B, a superantigen Nature 359:801-806(1992).
 RL


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QY      15 VLVTFLGLTIS-QEVEFAQODPD--PSQLHRSS-LVKNLQNIFYLFEGDPVTHENVK
Db      :|: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      71 LLSHHLIYNVSG---PNYDKLATKLNOEMATLFKDKNDVDIYGVEYYHLCYLCL--E
Db      :|: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      71 FLAHLDIYNISDKLKLYDKVKTLLNEDLAKKYADEVDVIGSNYYNCVFSSKK-
Db      :|: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      126 ----SACIYGGVNTHEGHNLETP--KKIVKVSIDIGIOSLSFDIETNKMKWTAQEL
Db      :|: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      131 VTGGTKTYMGGITKEGHNFDFNGNLQNVLRVRYENKRNTISFEVTDKKSVAQEL
Db      :|: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      180 RXYLDNKOLYNGSKYETGVIKRIPNKESFWDFFPEP--EFTOSKYLMIYKDR
Db      :|: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      191 RNFLINKNLYEFNSPYETGVIKRFIENNNGTNFWDMMPADPGDKFDQS KYLEMMDIN
Db      :|: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      238 DNSTSQIEVILTTK 251
Db      || : |||:|||||

251 DSKSVKIEVHLTTK 264

RESULT 4
ETC2_STAAB
ID ETC2_STAAB STANDARD; PRT; 266 AA.
AC P34071;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Enterotoxin type C-2 precursor (SEC2).
GN EMTC2.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcu.
OX NCBI_taxID=1280;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
RX MEDLINE=89277549; PubMed=2543637;
RA Bohach G.A., Schlievert P.M.;
RT "Conservation of the biologically active portions of staphylococcal
RT enterotoxins C1 and C2."
RL Infect. Immun. 57:2249-2252(1989).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=96027099; PubMed=7582894;
RA Papageorgiou A.C., Acharya K.R., Shapiro R., Passalacqua E.F.,
RA Brehm R.D., Tranter H.S.;
RT "Crystal structure of the superantigen enterotoxin C2 from
RT Staphylococcus aureus reveals a zinc-binding site."
RL Structure 3:769-779(1995).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=96022987; PubMed=7552730;
RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
RT "Residues defining V beta specificity in staphylococcal
RT enterotoxins."
RL Nat. Struct. Biol. 2:680-686(1995).
RN [4]
RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE=97334373; PubMed=9191070;
RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
RT "A structural and functional comparison of staphylococcal
RT enterotoxins A and C2 reveals remarkable similarity and
RT dissimilarity."
RL J. Mol. Biol. 269:270-280(1997).
CC CC -! COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC CC for the toxin interaction with MHC class II.
CC CC -! SUBCELLULAR LOCATION: Secreted.
CC CC -! DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC CC -! SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC CC FAMILY.
PR DR PIR: A60114; A60114.
DR DR PDB: 1STWF. 23-Dec-04

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Query Match 41.6%; Score 550.5; DB 1; Length 266;
Best Local Similarity 46.1; Pred. No. 8.3e-35;
Matches 117; Conservative 46; Mismatches 74; Indels 17; Gaps 8;

	Query Match	41.4%	Score 548;	DB 1;	Length 266;
	Best Local Similarity	44.1%;	Pred. No.	1.3e-34;	
	Matches 113; Conservative	52;	Mismatches	73;	Indels 18; Gaps 8;
QY	11 MVF-FVLVFLGLTISQEVFAQQDPSPQLHRSS-LVKNLQNLYFYLEGDPTVENKVS	68	:	: :	:: :
Dd	12 LIPALILVFLLTPNWLAE---SQDDPPIDELHKSEFTGTGMGNMKYLKDHHYSATRKMSV	68	:::	:	:
QY	69 DQLSLHLLIYNVSG----PNYDKLTKLKNOEMATLFKDNKVDTIGVEYYHLCLYC--ENA	123	:	:	:

Query Match 41.3%; Score 547; DB 1; Length 266;
Best Local Similarity 44.5%; Pred. No. 1.5e-34;
Matches 114; Conservative 51; Mismatches 73; Indels 18; Gaps 8;
QY 11 MVE-FVLVFLGLTISQEVFAQQDDPDSQLHRSSLYKNL-QNIYFLYEGDPVTHENVKSV 68
DB 12 LIPALLILVFTPNVLAEE---SQDPTPDELHKASKFTGLMNNKVLDDHYVSATKVKSV 68
QY 69 DQLLSHLIYNVSG---PNYDKLTKLKNQEMATLFDKNVDIYGYEYHLCVLC--ENA 123
DB 69 DKFLADLIYNISDKKLNKYDKVKTLLNEGLAKKYKDEVDVYGSYNYVNCYFSSKDNV 128
QY 124 ER-----SACIYGGVTNHEGHNHLEIP--KKIVKVSIDIGISLFSFIETNKKMVTQAQELDY 177
DB 129 GKVTGKTCMYGGITRKHGHNHFDNGNLQNVLIYENKRNITISFEVOTDKSVTAQELDI 188
QY 178 KVRKYLTDNKLTYNGSKYETGYIKFIPKNKESFWDFEPEP--EFTOSKYLMIYKDNE 235
DB 189 KARNFLINKNLKLYFNSSPYETGYIKFIENNGNTFWYDMAPDGFQDSKYLMIYNDNK 248
QY 236 TLDSNTSQIEVLYTTK 251
DB 249 TVDSKSVKLEVLHTTK 264

RESULT 6
ETXG_STAAU STANDARD; PRT; 258 AA.
AC 085382;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Enterotoxin type G precursor (SEG).
GN ENTG OR SEG OR SAV1824 OR SAV1642.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
OS Staphylococcus aureus.
OS Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158879, 1280;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN-FR1572;
RX MEDLINE=98298056; PubMed=9632603;
RA Munson S.H., Tremaine M.T., Betley M.J., Welch R.A.;
RT "Identification and characterization of staphylococcal enterotoxin
types G and I from Staphylococcus aureus";
RL Infect. Immun. 66:3337-3348(1998).
RN [2]

SEQUENCE FROM N.A.
RP STRAIN-Mu50 / ATCC 700699, and N315;
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.

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CC EMBL; AF064773; AAC26660.1; -;
CC DR EMBL; AP003363; BAB57986.1; -;
DR EMBL; AF003135; BAB42910.1; -;
DR PIR; G89968; G89968.
DR HSSP; P01552; ISBB.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1. Complete proteome.
KW Enterotoxin; Toxin; Signal; Superantigen; Complete proteome.
FT SIGNAL 1 25
FT CHAIN 26 258 BY SIMILARITY.
FT DISULFID 116 133
SQ SEQUENCE 258 AA; 29940 MW; E2982101701D012C CRC64;
Query Match 36.3%; Score 480; DB 1; Length 258;
Best Local Similarity 40.7%; Pred. No. 1.7e-29;
Matches 105; Conservative 46; Mismatches 91; Indels 16; Gap
QY 8 LKKMVFVLVTLFGLTISQEVFAQQDDP--SQLHRSSLYKN-----LQNIYFLYEGDP
DB 1 MKKLSTVILILILEIVFHNMYVNAQDPKLDLKNKVSIDYKKNKGTGNNVNLVTSPP
QY 62 HENVKSVQDLSHLIYNVSGPNYDKLTKLKNQEMATLFDKNVDIYGYEYHLCVLC
DB 61 GRGVINSRQFLSHDLIFPIEYKSYNEVKTELENTLANNYKDKKVDIFGVYFTCTII
QY 122 NAE-----RSACIYGGVTNHEGHNHLEIPKVIKVSIDIGISLFSFIETNKKMVTQAQ
DB 121 SEPDINQNFQGCCMYGGLTFNSEN-ERDKLITVQVITIDNRQSLGFTITTNKMMVTCII
QY 176 DYKVRKYLTDNKLTYNGSKYETGYIKFIPKNKESFWDFEPEP---FTOSKYLMIY
DB 180 DYKARHLTKERKLYEFDGSAFSGYIKFTEKNNTSFWFDLPKKELVDFVPYKFLNI
QY 233 DNETLDSNTSQIEVLYTT 250
DB 240 DNKVDKSIKMEVFLNT 257
RESULT 7
ETXD_STAAU STANDARD; PRT; 258 AA.
AC P20723;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Enterotoxin type D precursor (SED).
GN ENTG.
OS Staphylococcus aureus.
OX Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89359112; PubMed=2549000;
RA Bayles K.W., Iandolo J.J.;
RT "Genetic and molecular analyses of the gene encoding staphylococcal
enterotoxin D";
RL J. Bacteriol. 171:4799-4806(1989).
RN [2]
RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RC STRAIN-ATCC 23235;
RX MEDLINE=97157473; PubMed=9003758;
RA Sundstroem M., Abrahmsen L., Antonsson P., Mehindate K., Mourad W.,
RA Dohlstien M.;
RT "The crystal structure of staphylococcal enterotoxin type D reveals

QY 235 ETLD-SNTSQIEVYL 248
:: | | :||
Db 219 RIINMFNFHDIYL 233

RESULT 11
SPHE_STRPY STANDARD; PRT; 236 AA.

AC Q9X5C8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Exotoxin type H precursor (SPE H).
GN SPEP OR SPY1008.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
ON NCBI_TaxID=1314;
OX [1]
PC STRAIN=FROM N.A.
RC STRAIN=M15;
RX MEDLINE=99093428; PubMed=9874566;
RT Prof. T., Moffatt S.L., Berkahn C.J., Fraser J.D.;
RT "Identification and Characterization of novel superantigens from
RT Streptococcus pyogenes";
RL J. Exp. Med. 189:89-102(1999).
RP [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SR370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savić G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC -1- SUBUNIT: Binds to major histocompatibility complex class II beta
CC chain.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: Mitogenic for human peripheral blood lymphocytes.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC -----
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CC -----
DR EMBL; AF124500; AAD30989.1; -
DR EMBL; AE006546; AAK33907.1; -
DR PDB; 1ET9; 24-MAY-00.
DR PDB; 1EU4; 24-MAY-00.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_Ob.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Toxin; Signal; Complete proteome; 3D-structure.
FT SIGNAL 1 32
FT FT CHAIN 33 236 POTENTIAL.
FT FT CHAIN 33 236 EXOTOXIN TYPE H.
SQ SEQUENCE 236 AA; 27485 MW; 16352923907AD40D CRC64;

Query Match 16.1%; Score 213.5; DB 1; Length 236;
Best local Similarity 29.3%; Pred. No. 2.3e-09;
Matches 72; Conservative 36; Mismatches 113; Indels 23; Gaps 9;

QY 8 LKRMFVLVLTFLGITSQVFAQDPDPSQIHRSSIVKLNLIYFLYEGDPTVHNKVS 67


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DR PRINTS; PRO0279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Toxin; Signal; Complete proteome.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 234 EXOTOXIN TYPE G.
SQ SEQUENCE 234 AA; 27262 MW; 49525C49E4BA2052 CRC64;

Query Match 12.2%; Score 162; DB 1; Length 234;
Best Local Similarity 24.1%; Pred. No. 1.8e+05;
Matches 53; Conservative 42; Mismatches 81; Indels 44; Gaps 10;

QY 63 ENKSVQDLLSHLHLYNVSGPNYDK-----LKTCLKNQDMA----- 98
Db 26 ENLKDLKRSI--RFAYNITPCDYENVEIAFVNTSHINTKQRSECLYVDSIVSLGIT 83
QY 99 -TLFRDKNVDYIGVEYHYLCYLCENAESACIYGGVTNH--EGNHLEIPKKIWKVKSIDG 155
Db 84 DQFIKDGKVDVFGLPYFNFPYVDN-----YGGIVKHSNOGK---SLQFVGILNQDG 134
QY 156 IQSL--SFDIETNKQMTVAQELDYKVKYLTNKNQLYTNGPSKYETGYTKFIPKNKESFW 213
Db 135 KETLYLSEAVRIKKKQFTLQEFDFKIRKFLMEKYNII-DSERYTSGSLFLATKDSKHYE 193
QY 214 FDFPPEPE--FTQSKYLMYIKDNETLDS-NTSQIEVYLTT 250
Db 194 VDLFNKDDKLLSRDSFFKRYKDKNIPNSEEISHFDIYLKT 233.

TST.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RZ SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=87057222; PubMed=3782030;
RA Blomster-Hautamaa D.A., Kreiswirth B.N., Kornblum J.S., Novick R.P.,
RA Schlivert P.M.;
RT "The nucleotide and partial amino acid sequence of toxic shock
RL syndrome toxin-1.";
RL J. Biol. Chem. 261:15783-15786(1986).
RN [2]
RZ X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=94150598; PubMed=8107781;
RA Acharya K.R., Passalacqua E.F., Jones E.Y., Harlos K., Stuart D.I.,
RA Brehm R.D., Tranter H.S.;
RT "Structural basis of superantigen action inferred from crystal
RL structure of toxic-shock syndrome toxin-1.";
RL Nature 367:94-97(1994).
RN [3]
RZ X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=94092653; PubMed=8268150;
RA Prasad G.S., Earhart C.A., Murray D.L., Novick R.P., Schlivert P.M.,
RA Ohlendorf D.H.;
RT "Structure of toxic shock syndrome toxin 1.";
RL Biochemistry 32:13761-13766(1993).
RN [4]
RZ X-RAY CRYSTALLOGRAPHY (2.07 ANGSTROMS).
RX MEDLINE=96319751; PubMed=8759320;
RA Papageorgiou A.C., Brehm R.D., Leonidas D.D., Tranter H.S.,
RA Acharya K.R.;
RT "The refined crystal structure of toxic shock syndrome toxin-1 at
RL 2.07-A resolution.";
RL J. Mol. Biol. 260:553-569(1996).
RN [5]

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